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# OM protein - protein search, using sw model

Run on: November 8, 2005, 20:40:37 ; Search time 165 Seconds  
(without alignments)  
447.704 Million cell updates/sec

Title: US-09-805-354-1  
Sequence: 1 CPQEDSDIAFLIDSGSIIP.....VNFEALKTIONQREKKFA 191

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_1Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	974	99.8	194	8	ADR23221 Human int
2	974	99.8	1152	8	ADM95589 Human int
3	974	99.8	1152	8	ADP12435 Protein e
4	974	99.8	1153	2	AAR04136 Alpha sub
5	974	99.8	1153	2	AAW65090 Human Bet
6	974	99.8	1153	3	AAU07360 Human CDI
7	974	99.8	1153	5	ABG61469 Human int
8	974	99.8	1153	5	ABG61469 Human Bet
9	974	99.8	1153	7	AA014428 Integrin
10	974	99.8	1153	7	ADD25615 Binding d
11	974	99.8	1153	8	ADR23250 Human int
12	974	99.8	191	5	AAU76856 Human int
13	974	99.8	191	5	AAU76847 Human int
14	974	99.8	187	2	AAV21991 Human com
15	974	99.8	216	4	AAW65102 Mouse alp
16	974	99.8	435	2	AAW73344 Rat alp
17	974	99.8	177	5	AAU76865 Human int
18	974	99.8	177	5	AAU76865 Human int
19	974	99.8	199	5	AAU76872 Murine I-
20	974	99.8	1151	2	AAW23059 Rat beta
21	974	99.8	1151	2	AAW60001 Rat alpha
22	974	99.8	1151	2	AAW65101 Rat beta
23	974	99.8	1151	2	AAW72834 Rat alp
24	974	99.8	1151	2	AAW73344 Rat alp
25	974	99.8	1151	3	AAW73371 Rat alp

26	603	61.8	1151	5	ABG61480	ABG61480 Rat beta2
27	603	61.8	1161	2	AAW78169	AAW78169 Rat alp
28	603	61.8	1161	2	AAW23062	AAW23062 Rat beta
29	603	61.8	1161	2	AAW60004	AAW60004 Rat alp
30	603	61.8	1161	2	AAW65104	AAW65104 Rat beta-
31	603	61.8	1161	2	AAW72824	AAW72824 Rat alp
32	603	61.8	1161	2	AAW73345	AAW73345 Rat alp
33	603	61.8	1161	3	AAW07374	AAW07374 Rat alp
34	603	61.8	1161	5	ABG61483	ABG61483 Rat beta2
35	602	61.7	413	2	AAW23065	AAW23065 Rabbit be
36	602	61.7	413	2	AAW65107	AAW65107 Rabbit be
37	602	61.7	413	2	AAW72839	AAW72839 Rabbit al
38	602	61.7	413	2	AAW73348	AAW73348 Rabbit al
39	602	61.7	413	3	AAW07377	AAW07377 Rabbit al
40	602	61.7	1151	2	AAW78179	AAW78179 Rat alp
41	600	61.5	413	5	ABG61486	ABG61486 Rabbit Be
42	594	60.9	1155	2	AAW78167	AAW78167 Mouse alp
43	594	60.9	1155	2	AAW23060	AAW23060 Mouse bet
44	594	60.9	1155	2	AAW60002	AAW60002 Mouse alp
45	594	60.9	1155	2	AAW65102	AAW65102 Mouse bet

## ALIGNMENTS

RESULT 1  
ID ADR23221 standard; protein; 194 AA.  
XX  
AC ADR23221;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Human integrin CD11b alpha subunit A domain.  
XX  
KW Human; integrin; CD11b; inflammation; antiinflammatory; vasotropic.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 1..191  
FT MISC-difference 189 /label = A\_domain  
FT MISC-difference 189 /note= "Invariant Ile residue"  
XX  
XX WO2004066914-A2.  
XX PN 12-AUG-2004.  
XX PF 12-MAY-2003; 2003WO-US014919.  
XX PR 10-MAY-2002; 2002US-00144259.  
XX (GEHO ) GEN HOSPITAL CORP.  
XX Arnaout MA, Li R, Xiong J;  
XX WPI; 2004-593980/57.  
XX  
XX Novel variant integrin CD11b alpha subunit polypeptide, useful for  
XX determining candidate compound for binding to CD11b, and for determining  
XX compound as activation-dependent ligand.  
XX  
XX Disclosure; SEQ ID NO 1; 128pp; English.  
XX  
XX The present sequence is that of the human integrin alpha subunit CD11b A  
XX domain. This includes an invariant Ile residue. The invention features  
XX variant integrin alpha subunit polypeptides in which the invariant Ile is  
XX substituted by Gly, Ala or some other amino acid (e.g. Val) or is  
XX deleted. The polypeptide can include part or all of the A domain.  
XX Replacing the invariant Ile creates a variant integrin polypeptide that  
XX is more active (i.e. in solution has a greater proportion of ligand-  
XX forming polypeptides) than the wild-type form of the subunit. Variant

CC Integrin polypeptides of the invention are useful in assays for compounds  
CC that bind to a variant ligand, that interfere with or enhance the binding  
CC of an integrin ligand to integrin, and for identifying activation-  
CC specific ligands. They are also useful for generating antibodies, e.g.  
CC monoclonal antibodies, which bind to the high efficiency form of an  
CC integrin. Some such antibodies recognise an epitope that is either not  
CC present or not accessible on an integrin that is in a lower affinity  
CC conformation. The invention also provides methods of administering a  
CC variant integrin polypeptide, or an antibody that selectively binds it,  
CC to identify a ligand which binds to an active integrin. Such assays are  
CC useful for diagnosing inflammation, e.g. occult inflammation (e.g.  
CC abscess or an active arteriosclerotic lesion). Variant integrin  
CC polypeptides can also be used to affect the bioavailability of a variant  
CC integrin polypeptide ligand and to treat disorders associated with  
CC aberrant or unwanted integrin expression or activity, such as vascular  
CC injury.

CC SQ Sequence 194 AA;

Query Match 99.8%; Score 974; DB 8; Length 194;  
Best Local Similarity 99.5%; Pred. No. 5.4e-99;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQLKSKTLPFLMOYSEEFRIHFPEK 60  
DB 1 CPQEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQLKSKTLPFLMOYSEEFRIHFPEK 60  
QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120  
DB 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120  
QY 121 DPLGEDVIPLEADREGVIRVYIGVDARFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
DB 121 DPLGEDVIPLEADREGVIRVYIGVDARFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
QY 181 IQNQLREKIFA 191  
DB 181 IQNQLREKIFA 191

RESULT 2

ADM99589 ADM99589 standard; protein; 1152 AA.

AC ADM99589;  
XX  
DT 17-JUN-2004 (first entry)

XX Human integrin alphaM subunit precursor protein.

XX integrin alpha subunit; beta; antiproliferative; thrombolytic; anticoagulant;  
KW osteoplastic; cytosolic; immunosuppressive; antiinflammatory;  
KW neuroprotective; antisticking; immunotherapy; inflammatory;  
KW autoimmune disorder; thrombosis; cancer; osteoporosis;  
KW sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;  
KW alphaM.

XX Homo sapiens.

XX Key Location/Qualifiers  
FT Misc-difference 965  
FT /note="Encoded by CCC"

XX MO2004007530-A2.

XX 22-JAN-2004.

XX 17-JUL-2003; 2003WO-US022301.

XX 17-JUL-2002; 2002US-0396783P.

XX 17-JUL-2002; 2002US-0396790P.

XX 11-SEP-2002; 2002US-0410135P.

PA (BL00-) CENT BLOOD RES INC.

XX Springer TA, Takagi J;

XX WPI; 2004-122877/12.

DR N-PSDB; ADM99589.

XX Novel modified integrin protein having extracellular domains of integrin  
PT alpha and beta subunits or integrin alphaII and beta3 subunit, useful for  
PT treating integrin mediated disorders.

XX Disclosure; SEQ ID NO 4; 232dp; English.

PS The invention relates to a novel isolated or recombinant modified  
CC integrin protein having extracellular domains of integrin alpha and beta  
CC subunits where one of the subunits has one or more mutations, an altered  
CC surface feature or an amino acid substitution or internal deletion,  
CC extracellular domains of the integrin beta subunit that comprise a  
CC mutation that alters a non-cysteine residue to cysteine or extracellular  
CC domains of integrin alpha and beta subunits. The polypeptide of the  
CC invention demonstrates antiproliferative, thrombolytic, anticoagulant,  
CC osteoplastic, cytosolic, immunosuppressive, antinflammatory,  
CC neuroprotective and antisticking activities and may be useful for  
CC immunotherapy in order to prevent or treat an integrin-mediated disorder  
CC such as an inflammatory disorder, an autoimmune disorder, thrombosis,  
CC cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple  
CC sclerosis. The current sequence is that of the human integrin alphaM  
CC subunit precursor protein of the invention.

XX SQ Sequence 1152 AA;

Query Match 99.8%; Score 974; DB 8; Length 1152;  
Best Local Similarity 99.5%; Pred. No. 6.5e-98;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQLKSKTLPFLMOYSEEFRIHFPEK 60  
DB 144 CPQEDSDIAFLIDSGSIIIPHDFRMKEFVSTVMEQLKSKTLPFLMOYSEEFRIHFPEK 203  
QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120  
DB 204 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 263  
QY 121 DPLGEDVIPLEADREGVIRVYIGVDARFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
DB 264 DPLGEDVIPLEADREGVIRVYIGVDARFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
QY 181 IQNQLREKIFA 191  
DB 324 IQNQLREKIFA 334

RESULT 3

ADP12435 ADP12435 standard; protein; 1152 AA.

XX ADP12435;

XX 12-AUG-2004 (first entry)

XX Protein encoded by mRNA of the invention #45.

XX transplant rejection; immune system; rheumatoid arthritis; lupus;  
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.

XX Homo sapiens.

XX MO2004042346-A2.

XX 21-MAY-2004.

XX 24-APR-2003; 2003WO-US012946.



SC Sequence 1153 AA;  
Query Match 99.8%; Score 974; DB 2; Length 1153;  
Best Local Similarity 99.5%; Pred. No. 6.5e-98;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKKSKTLFSLMOYSEEFRIHPTFK 60  
DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKKSKTLFSLMOYSEEFRIHPTFK 203  
OY 61 EFQNNPNRSLVKEPTTOLLGRTHATGIRKVVRELFTNTNGARKNAFKILVITDGEKFG 120  
DB 204 EFQNNPNRSLVKEPTTOLLGRTHATGIRKVVRELFTNTNGARKNAFKILVITDGEKFG 263  
OY 121 DPLGVEDVIPPADREGVIRVYIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
DB 264 DPLGVEDVIPPADREGVIRVYIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
OY 181 IQNQLREKXFA 191  
DB 324 IQNQLREKXFA 334  
RESULT 5  
AAM65090  
ID AAM65090 standard; protein; 1153 AA.  
XX AC AAM65090;  
XX DT 28-SEP-1998 (first entry)  
XX DE Human Beta-integrin CD11b subunit protein.  
XX KM Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis;  
XX KM type-I diabetes; atherosclerosis; multiple sclerosis; asthma;  
XX KM lung inflammation; acute respiratory distress syndrome; CD11b subunit;  
XX KM rheumatoid arthritis.  
XX OS Homo sapiens.  
XX PN US5728533-A.  
XX PD 17-MAR-1998.  
XX PF 07-JUN-1995; 95US-00485618.  
XX PR 23-DEC-1993; 93US-00173497.  
XX PR 05-AUG-1994; 94US-00286889.  
XX PR 21-DEC-1994; 94US-00362652.  
XX PA (ICOS-) ICOS CORP.  
XX PI Van Der Vlieten M, Gallatin MM;  
XX DR WPI; 1998-206565/18.  
XX PT Screening assay for modulators of integrin binding - using immobilised or  
XX PT labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.  
XX PS Example 5; Fig 1A-D; 106pp; English.  
XX CC This sequence represents a human beta-integrin CD11b subunit which is  
XX CC used to describe a method for identifying compounds that modulate the  
XX CC interaction of the beta-integrin alpha-d subunit with a binding partner  
XX CC of alpha-d which involves contacting an alpha-d polypeptide with an alpha  
XX CC -d binding partner, one of which is immobilised and the other of which is  
XX CC labelled, in the presence of a test compound, and determining if the  
XX CC compound affects binding between the alpha-d polypeptide and alpha-d  
XX CC binding partner, where the alpha-d polypeptide is alpha-d or its fragment  
XX CC comprising the cytoplasmic, transmembrane or extracellular domain of  
XX CC alpha-d. Compounds that modulate alpha-d binding could be used to treat  
XX CC diseases such as type-I diabetes, atherosclerosis, multiple sclerosis,  
XX CC asthma, psoriasis, lung inflammation, acute respiratory distress syndrome

CC and rheumatoid arthritis  
XX SQ Sequence 1153 AA;  
Query Match 99.8%; Score 974; DB 2; Length 1153;  
Best Local Similarity 99.5%; Pred. No. 6.5e-98;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKKSKTLFSLMOYSEEFRIHPTFK 60  
DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKKSKTLFSLMOYSEEFRIHPTFK 203  
OY 61 EFQNNPNRSLVKEPTTOLLGRTHATGIRKVVRELFTNTNGARKNAFKILVITDGEKFG 120  
DB 204 EFQNNPNRSLVKEPTTOLLGRTHATGIRKVVRELFTNTNGARKNAFKILVITDGEKFG 263  
OY 121 DPLGVEDVIPPADREGVIRVYIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
DB 264 DPLGVEDVIPPADREGVIRVYIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
OY 181 IQNQLREKXFA 191  
DB 324 IQNQLREKXFA 334  
RESULT 6  
AAB07360  
ID AAB07360 standard; protein; 1153 AA.  
XX AC AAB07360;  
XX DT 17-JAN-2001 (first entry)  
XX DE Human CD11b protein sequence.  
XX KM Human; macrophage infiltration inhibition; alpha-d integrin;  
XX KM leukocyte integrin; Leu-CAM; leukointegrin; immune response;  
XX KM inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes;  
XX KM atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin;  
XX KM lung inflammation; acute respiratory distress syndrome; Crohn's disease;  
XX KM rheumatoid arthritis; central nervous system injury; CD11b.  
XX OS Homo sapiens.  
XX PN WO200029446-A1.  
XX PD 25-MAY-2000.  
XX PF 16-NOV-1999; 99WO-USO27139.  
XX PR 16-NOV-1998; 98US-00193043.  
XX PR 08-JUL-1999; 99US-00350259.  
XX PA (ICOS-) ICOS CORP.  
XX PI Gallatin MM, Van Der Vlieten M;  
XX DR WPI; 2000-387751/33.  
XX PT Use of novel anti-alpha integrin d monoclonal antibodies to inhibit  
XX PT macrophage infiltration and reduce inflammation at central nervous system  
XX PT injury sites.  
XX PS Example 5; Fig 1; 270pp; English.  
XX CC Integrins are a class of membrane-associated molecules that participate  
XX CC in cellular adhesion. Integrins are made up of an alpha subunit and a  
XX CC beta subunit. One class of human integrins are restricted to expression  
XX CC in white blood cells and have a common beta2 subunit: the leukocyte  
XX CC integrins, Leu-CAMe, leukointegrins or beta2 integrins. Beta2 integrins  
XX CC have an important role in immune and inflammatory responses. The present  
XX CC protein sequence is the human integrin alpha subunit CD11b. This sequence  
XX CC was used in an alignment to identify a novel beta2 integrin alpha

CC subunit: alpha\_d (AA60014 and AAB07359). The present sequence has  
 CC approximately 60% identity to the protein sequence of alpha\_d. The  
 CC Alpha\_d gene and protein may be useful in therapy for diseases linked to  
 CC aberrant alpha\_d function e.g. Type I diabetes, atherosclerosis, multiple  
 CC sclerosis, asthma, psoriasis, lung inflammation, acute respiratory  
 CC distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency  
 CC (LAD). In addition, anti-alpha\_d monoclonal antibodies may be used in the  
 CC inhibition of macrophage infiltration at the site of a central nervous  
 CC system injury. The monoclonal antibodies can also be used to detect and  
 CC diagnose Crohn's disease

XX Sequence 1153 AA:

Query Match 99.8%; Score 974; DB 3; Length 1153;

Best Local Similarity 99.5%; Pred. No. 6.5e-98;

Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHPFRMKKEVSTVMEQLKSKTLFSLMOYSEEFRIHFTPK 60  
 DB 144 CPQEDSDIAFLIDGSGSIIPHPFRMKKEVSTVMEQLKSKTLFSLMOYSEEFRIHFTPK 203  
 QY 61 EFQNNPNPSLVKPIITQLGRTHTATGIRKVRLEFNITNGARKNAFKILVITDGEKFG 120  
 DB 204 EFQNNPNPSLVKPIITQLGRTHTATGIRKVRLEFNITNGARKNAFKILVITDGEKFG 263  
 QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTASKPPRDHVFQVNNFEALKT 180  
 DB 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTASKPPRDHVFQVNNFEALKT 323  
 QY 181 IONQLREKKFA 191  
 DB 324 IONQLREKKIFA 334

#### RESULT 7

AAU80252  
 ID AAU80252 standard; protein; 1153 AA.

XX AAU80252;

AC 15-JUL-2002 (first entry)

DE Human integrin 1 alpha-M subunit protein.

XX Integrin: antiinflammatory; immunosuppression; nephritis; dermatitis;

KW inflammatory disease; autoimmune disorder; Crohn's disease;

KW human immunodeficiency virus; HIV; myocardial infarction;

KW Sjorgen's syndrome; rheumatoid arthritis.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Misc-difference 499.500

XX /note="Encoded by GCG CAG AGC"

XX MO200218583-A2.

XX 07-MAR-2002.

XX 31-AUG-2001; 2001MO-US027227.

XX 01-SEP-2000; 2000US-0229700P.

XX (BLOO-) CENT BLOOD RES INC.

XX Springer TA, Shimooka M, Lu C;

XX WPI; 2002-382964/41.

XX N-PSDB; ABKS0046.

XX Modified integrin-I or integrin I-like domain polypeptide useful as an

PT immunogen to produce antibodies specific to polypeptide, comprises a

PT disulfide bond such that polypeptide is stabilized in a desired

PT conformation.

XX Disclosure; Page 109-112; 112pp; English.

XX This invention relates to a modified integrin-I or integrin I-like domain  
 PS polypeptide comprising at least one disulfide bond so that the domain is  
 CC stabilised in a desired conformation. The polypeptide of the invention  
 CC may have antiinflammatory or immunosuppressive activities. The  
 CC polypeptides of the invention have an open conformation and are useful as  
 CC immunogens to produce antibodies that selectively bind to integrin I-  
 CC domain; and for identifying a modulator of integrin activity, or of the  
 CC interaction of an integrin and a cognate ligand. The polypeptide of the  
 CC invention, or antibodies (preferably anti-LPA-1 antibody) is useful for  
 CC treating or preventing an integrin mediated disorder which is an  
 CC inflammatory or autoimmune disorder in a subject and for inhibiting the  
 CC binding of an integrin to a cognate ligand such as Crohn's disease,  
 CC nephritis; human immunodeficiency virus (HIV), myocardial infarction,  
 CC Sjorgen's syndrome, rheumatoid arthritis, dermatitis. A therapeutic  
 CC composition comprising the peptide of the invention is useful for  
 CC treating an integrin mediated disorder in a subject. The polypeptides  
 CC and/or active or antigenic fragments are useful as reagents for diagnosis  
 CC of integrin-mediated disorders. The present sequence represents the human  
 CC integrin-1 alpha-M protein subunit used to generate the mutant  
 CC polypeptides of the invention

XX Sequence 1153 AA:

Query Match 99.8%; Score 974; DB 5; Length 1153;

Best Local Similarity 99.5%; Pred. No. 6.5e-98;

Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHPFRMKKEVSTVMEQLKSKTLFSLMOYSEEFRIHFTPK 60  
 DB 144 CPQEDSDIAFLIDGSGSIIPHPFRMKKEVSTVMEQLKSKTLFSLMOYSEEFRIHFTPK 203  
 QY 61 EFQNNPNPSLVKPIITQLGRTHTATGIRKVRLEFNITNGARKNAFKILVITDGEKFG 120  
 DB 204 EFQNNPNPSLVKPIITQLGRTHTATGIRKVRLEFNITNGARKNAFKILVITDGEKFG 263  
 QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTASKPPRDHVFQVNNFEALKT 180  
 DB 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTASKPPRDHVFQVNNFEALKT 323  
 QY 181 IONQLREKKFA 191  
 DB 324 IONQLREKKIFA 334

#### RESULT 8

ABG61469  
 ID ABG61469 standard; protein; 1153 AA.

XX ABG61469;

AC 27-AUG-2002 (first entry)

DE Human Beta2 integrin alphaCD11b subunit;

XX Beta2 integrin; alphasubunit; CD11c subunit; CD11b subunit; LAD;

KW leukocyte adhesion deficiency; inflammatory response; diabetes;

KW multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective;

KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;

KW immune complex alveolitis; leukemia; ICAM-R; VCM-1; anti-inflammatory;

KW intracellular cell adhesion molecule; vascular cell adhesion molecule;

KW locomotor recovery; locomotor damage; locomotor impairment;

XX autonomic dysfunction; sensory dysfunction; spinal cord injury.

XX Homo sapiens.

XX MO200230980-A2.

XX 18-APR-2002.

PF 15-OCT-2001; 2001WO-US032059.  
 XX 13-OCT-2000; 2000US-00688307.  
 PR  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 XX  
 PI Gallatin WM, Van Der Vlieten M;  
 XX  
 DR WPI; 2002-463260/49.  
 XX

PT Use of an anti-alpha-d monoclonal antibodies for promoting locomotor  
 recovery, inhibiting locomotor damage, limiting locomotor impairment, or  
 PT limiting autonomic and sensory dysfunction following spinal cord injury.  
 XX  
 XX

Example 5; Page 191-194; 270pp; English.

CC The invention relates to promoting locomotor recovery, inhibiting  
 CC locomotor damage, limiting locomotor impairment, or limiting autonomic  
 CC and sensory dysfunction following spinal cord injury by administering an  
 CC anti-alpha-d (beta2 integrin alpha2 subunit) monoclonal antibody to a  
 CC spinal cord injury victim. The method also involves the use of a ligand  
 CC selected from ICM-R or VCM-1 (intracellular cell adhesion molecule,  
 CC vascular cell adhesion molecule). The method is useful for promoting  
 CC locomotor recovery, inhibiting locomotor damage, limiting locomotor  
 CC impairment, or limiting autonomic and sensory dysfunction following  
 CC spinal cord injury. In particular, the spinal cord injury comprises  
 CC compression of the spinal cord. The antibodies are also useful for  
 CC reducing inflammation at the site of a central nervous system injury. The  
 CC specification also details the identification of beta2 integrin alpha2  
 CC cDNAs and proteins, for use in raising the antibodies. Beta2 integrins  
 CC are implicated in diseases such as LAD (leukocyte adhesion deficiency,  
 CC inflammatory response, diabetes, multiple sclerosis, arthritis, graft  
 CC atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative  
 CC colitis, immune complex alveolitis and leukemia. The present sequence is  
 CC a beta2 integrin alpha subunit sequence included for comparison with the  
 CC beta2 integrin alpha2 protein sequences  
 XX  
 XX

Sequence 1153 AA;

Query Match 99.8%; Score 974; DB 5; Length 1153;

Best Local Similarity 99.5%; Pred. No. 6.5e-98;

Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPDPRMKEFVSTVMEOLKSKTLPFLMOYSEEFRIHFTFK 60  
 DB 144 CPQEDSDIAFLIDSGSIIIPDPRMKEFVSTVMEOLKSKTLPFLMOYSEEFRIHFTFK 203  
 QY 61 EFQNNPNRSLVKPITTLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120  
 DB 204 EFQNNPNRSLVKPITTLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263  
 QY 121 DPLGVEDVTPADREGVIRYVIGVDAPFRSEKSRQELNTTASKPPRDHVPVNNFEALKT 180  
 DB 264 DPLGVEDVTPADREGVIRYVIGVDAPFRSEKSRQELNTTASKPPRDHVPVNNFEALKT 323  
 QY 181 IQNQLREKXFA 191  
 DB 324 IQNQLREKIFA 334

RESULT 9  
 AA014428  
 ID AA014428 standard; protein; 1153 AA.  
 XX  
 AC AA014428;

XX 03-MAY-2002 (first entry)

DE Integrin Mac-1 alpha subunit.

XX Mac-1; integrin alpha subunit; variant integrin inserted domain protein;  
 KM open conformation; integrin related inflammatory disorder;  
 KM integrin related immunological disorder; rheumatoid arthritis; ischaemia;  
 XX

KM reperfusion; hypovolemic shock; infarctbn; cerebral shock;  
 KM viral infection; cancer; gene therapy; vaccine;  
 KM bioactive agent screening.  
 XX  
 XX

OS Unidentified.

XX WO200204521-A2.

XX 17-JAN-2002.

PF 09-JUL-2001; 2001WO-US021805.

XX 07-JUL-2000; 2000US-0216600P.

PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
 PA (BLOO-) CENT BLOOD RES.  
 XX  
 XX

PI Springer T;

DR WPI; 2002-146167/19.

PT New integrin I domain protein having alteration in at least 2  
 PT noncontiguous regions and exits in an open conformation, useful for  
 PT treating, preventing or suppressing inflammatory or immunological  
 PT disorders.

XX Example 1; Fig 1F; 90pp; English.

XX The invention comprises structurally biased variant integrin inserted (I)  
 CC domain proteins, wherein the alterations to the protein occur in at least  
 CC two noncontiguous regions. Specifically the variant integrin I domain  
 CC proteins are structurally biased to exist in the open conformation,  
 CC thereby altering the binding ability of the protein. The invention also  
 CC comprises nucleic acids encoding the variant integrin I domain proteins.  
 CC The integrin I domain proteins and nucleic acids are useful for treating,  
 CC preventing or suppressing integrin related inflammatory and immunological  
 CC disorders (e.g. Rheumatoid arthritis). The variant integrin I domain  
 CC proteins and nucleic acids can also be used for treating: ischaemia/  
 CC reperfusion (e.g. hypovolemic shock); infarction; cerebral shock; viral  
 CC infection; and cancer. The variant integrin I domain nucleic acids and  
 CC proteins may be used in gene therapy, as vaccines and to screen for  
 CC bioactive agents. The present amino acid sequence represents the Mac-1  
 CC alpha subunit of integrin  
 XX  
 XX

Sequence 1153 AA;

Query Match 99.8%; Score 974; DB 5; Length 1153;

Best Local Similarity 99.5%; Pred. No. 6.5e-98;

Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPDPRMKEFVSTVMEOLKSKTLPFLMOYSEEFRIHFTFK 60  
 DB 144 CPQEDSDIAFLIDSGSIIIPDPRMKEFVSTVMEOLKSKTLPFLMOYSEEFRIHFTFK 203  
 QY 61 EFQNNPNRSLVKPITTLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120  
 DB 204 EFQNNPNRSLVKPITTLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263  
 QY 121 DPLGVEDVTPADREGVIRYVIGVDAPFRSEKSRQELNTTASKPPRDHVPVNNFEALKT 180  
 DB 264 DPLGVEDVTPADREGVIRYVIGVDAPFRSEKSRQELNTTASKPPRDHVPVNNFEALKT 323  
 QY 181 IQNQLREKXFA 191  
 DB 324 IQNQLREKIFA 334

RESULT 10  
 ADD25615  
 ID ADD25615 standard; protein; 1153 AA.  
 XX  
 AC ADD25615;

XX

15-JAN-2004 (first entry)  
 Binding domain-immunoglobulin fusion protein-associated protein #85.  
 Binding domain: immunoglobulin; fusion protein; cytosolic;  
 antileukemic; immunosuppressive; antidiabetic; antitumor;  
 neuroprotective; hinge region; immunoglobulin heavy chain;  
 CH2 constant region; CH3 constant region; IgG1;  
 antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
 malignant condition; B-cell disorder; melanoma; sarcoma;  
 rheumatoid arthritis; myasthenia gravis; Grave's disease;  
 type I diabetes mellitus; multiple sclerosis; autoimmune disease.  
 Unidentified.  
 US2003118592-A1.  
 26-JUN-2003.  
 25-JUL-2002; 2002US-00207655.  
 17-JAN-2001; 2001US-0367358P.  
 17-JUN-2002; 2002US-00653530.  
 03-JUN-2002; 2002US-0385691P.  
 (GENE-) GENE-CRAFT INC.  
 Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
 WPI; 2003-801317/75.  
 New binding domain-immunoglobulin fusion protein, useful for treating a  
 subject having or suspected of having a malignant condition or a B-cell  
 disorder, e.g. melanoma, Grave's disease or autoimmune disease.  
 Disclosure; SEQ ID NO 176; 157pp; English.  
 The invention relates to a binding domain-immunoglobulin fusion protein  
 comprising a binding domain polypeptide that is fused to an  
 immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
 CH2 constant region polypeptide that is fused to the hinge region  
 polypeptide, and an immunoglobulin heavy chain CH3 constant region  
 polypeptide that is fused to the CH2 constant region polypeptide. The  
 hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin  
 hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge  
 region polypeptide; derived from (a) having 3 or more cysteine residues;  
 where the mutated human IgG1 immunoglobulin hinge region polypeptide  
 contains 2 cysteine residues, where the first cysteine is not mutated; a  
 mutated human IgG1 immunoglobulin hinge region polypeptide; derived from  
 (a) having 3 or more cysteine residues, where the mutated human IgG1  
 immunoglobulin hinge region polypeptide contains no more than one  
 cysteine residue; and a mutated human IgG1 immunoglobulin hinge region  
 polypeptide; derived from (a) having 3 or more cysteine residues, where  
 the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
 no cysteine residues. The binding domain-immunoglobulin fusion protein is  
 capable of at least one immunological activity comprising antibody  
 dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
 binding domain polypeptide is capable of specifically binding to an  
 antigen. Also included are an isolated polynucleotide encoding the  
 binding domain-immunoglobulin fusion protein, a recombinant expression  
 construct comprising the polynucleotide (operably linked to a promoter),  
 a host cell transformed or transfected with a recombinant expression  
 construct, producing the binding domain-immunoglobulin fusion protein, a  
 pharmaceutical composition comprising the binding domain-immunoglobulin  
 fusion protein or polynucleotide and a carrier, and treating a subject  
 having or suspected of having a malignant condition or a B-cell disorder.  
 The binding domain-immunoglobulin fusion protein is useful for treating a  
 subject having or suspected of having a malignant condition or a B-cell  
 disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,  
 myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple  
 sclerosis or autoimmune disease. The present sequence is a binding domain  
 -immunoglobulin fusion protein-associated protein sequence. Note: The  
 sequence data for this patent formed part of the printed specification

and is also available in electronic format directly from USPTO at  
 cc segdata.uspto.gov/sequence.html?docid=20030118592. The authors have not  
 identified the sequences in the printed specification by their SEQ ID  
 number therefore none of the sequences can be explicitly identified.  
 SQ Sequence 1153 AA;  
 Query Match 99.8%; Score 974; DB 7; Length 1153;  
 Best Local Similarity 99.5%; Pred. No. 6,5e-98;  
 Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTPK 60  
 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTPK 203  
 61 EFQNNPNPRLSVKPTQLGRTHTATGIRKRVRELFINITNGARKNAFKLLVITDGEKFG 120  
 204 EFQNNPNPRLSVKPTQLGRTHTATGIRKRVRELFINITNGARKNAFKLLVITDGEKFG 263  
 121 DPLGYEDVTPEDRGVIRYVIGVDAPRSEKSRBELNTIASKPPRDHVFQVNFPEALKT 180  
 264 DPLGYEDVTPEDRGVIRYVIGVDAPRSEKSRBELNTIASKPPRDHVFQVNFPEALKT 323  
 181 IONOLREKKFA 191  
 324 IONOLREKIFA 334  
 Db  
 RESULT 11  
 ADR23250  
 ID ADR23250 standard; protein; 1153 AA.  
 AC ADR23250;  
 XX  
 DT 04-NOV-2004 (first entry)  
 XX  
 DE Human integrin CD11b alpha subunit.  
 XX  
 KW Human; integrin; CD11b; inflammation; antiinflammatory; vasotropic.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..16  
 FT Domain /label= Signal\_peptide  
 FT /label .334  
 FT /label = A\_domain  
 FT Misc-difference 332  
 FT /note= "Invariant Ile residue"  
 FT Misc-difference 336  
 FT /note= "Invariant Glu residue"  
 XX  
 PN WC2004066914-A2.  
 PD 12-AUG-2004.  
 XX  
 PF 12-MAY-2003; 2003WO-US014919.  
 PR 10-MAY-2002; 2002US-00144259.  
 XX  
 PA (GENO) GEN HOSPITAL CORP.  
 PI Arnaud MA, Li R, Xiong J;  
 XX  
 DR WPI; 2004-593980/57.  
 XX  
 PT Novel variant integrin CD11b alpha subunit polypeptide, useful for  
 determining candidate compound for binding to CD11b, and for determining  
 compound as activation-dependent ligand.  
 XX  
 PS Claim 4; SEQ ID NO 30; 128pp; English.  
 CC The present sequence is that of the human integrin alpha subunit CD11b.

CC This includes an invariant Ile residue at position 332 and an invariant  
 CC Glu residue at position 336. The invention features variant integrin  
 CC polypeptides comprising all or part of a variant integrin alpha subunit A  
 CC domain and its flanking region. In solution or in membrane-associated  
 CC form, the A domain polypeptides exist predominantly in a high affinity  
 CC conformation. The variant integrin polypeptides have a crucial Ile or Glu  
 CC residue either deleted or replaced by a different amino acid. Claimed  
 CC polypeptides comprise: amino acids 144-336 of the present CD11b alpha  
 CC subunit sequence in which the Glu-336 residue is replaced by Glu, Asp or  
 CC Ala; amino acids 144-332 of the CD11b alpha subunit where the Ile-332  
 CC residue is replaced by any other amino acid, especially Gly or Ala; and  
 CC amino acids 144-331 of the CD11b alpha subunit sequence, but not amino  
 CC acids 332-1152 of this sequence. The variant integrin polypeptides  
 CC selectively impair binding or activation-dependent ligands, but not  
 CC independent ligands. They are useful in screening assays for the  
 CC identification of molecules that enhances binding of variant polypeptides  
 CC with impaired binding, and for distinguishing between activation-  
 CC dependent and activation-independent ligands. They are also useful for  
 CC generating antibodies, e.g. monoclonal antibodies, which bind to the  
 CC impaired form of an integrin. Such antibodies recognise an epitope that  
 CC is either not present or not accessible on an integrin that is in the  
 CC high affinity conformation. The invention also provides methods of  
 CC administering a variant integrin polypeptide, or an antibody that  
 CC selectively binds it, to identify a ligand which binds to an active  
 CC integrin. Such assays are useful for diagnosing inflammation, e.g. occult  
 CC inflammation (e.g. abscess or an active arteriosclerotic lesion). Variant  
 CC integrin polypeptides can also be used to affect the bioavailability of a  
 CC variant integrin polypeptide ligand and to treat disorders associated  
 CC with aberrant or unwanted integrin expression or activity, such as  
 CC vascular injury.

CC Sequence 1153 AA:

Query Match 99.8%; Score 974; DB 8; Length 1153;  
 Best Local Similarity 99.5%; Pred. No. 6,5e-98;  
 Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTILFSIMQSEEFRIHFTFK 60  
 DB 144 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTILFSIMQSEEFRIHFTFK 203  
 QY 61 EFQNNPNPRSLVKPTITQLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120  
 DB 204 EFQNNPNPRSLVKPTITQLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 263  
 QY 121 DPLGYEDVIPADREGVIRVYIGVDAPFRSEKSRQELNTIASKPRDHVFOVNNFEALKT 180  
 DB 264 DPLGYEDVIPADREGVIRVYIGVDAPFRSEKSRQELNTIASKPRDHVFOVNNFEALKT 323  
 QY 181 IONQLREKXFA 191  
 DB 324 IONQLREKXFA 334

RESULT 12

AAU76856  
 ID AAU76856 standard; protein; 191 AA.

AC AAU76856;

DT 21-MAY-2002 (first entry)

DE Human integrin alpha subunit CD11b variant A domain.

XX Human, integrin alpha subunit; A domain; CD11b; integrin beta subunit;  
 KM A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;  
 KM ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;  
 KM antiinflammatory; vasotropic; antiparasitic; vulnery; gene therapy;  
 KM mutcin.

OS Homo sapiens.  
 OS Synthetic.  
 XX

FN Key Location/Qualifiers  
 FT Misc-difference 189  
 FT /label= Gly, Ala  
 FT /note= "wild-type Ile substituted by Gly or Ala"

PN WO200209737-A1.

PD 07-FEB-2002.

PF 31-JUL-2001; 2001WO-US023957.

XX 31-JUL-2000; 2000US-0221950P.

PR 11-JAN-2001; 2001US-00758493.

PR 13-MAR-2001; 2001US-00805354.

XX (GENO) GEN HOSPITAL CORP.

PI Arnaout AM, Li R, Xiong J;

DR WPI; 2002-188687/24.

PT Novel high affinity integrin polypeptide useful for treating restenosis  
 PT and parasitic diseases, comprises all or part of variant integrin alpha  
 PT subunit A domain or variant integrin beta subunit A-like domain.

PS Claim 2; Page; 55pp; English.

CC The invention relates to a high affinity integrin polypeptide comprising  
 CC all or part of a variant integrin alpha subunit A domain or a variant  
 CC integrin beta subunit A-like domain. The polypeptide, preferably the  
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by  
 CC G or A. F at residue 313 and A at residue 320 have been replaced by C, or  
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful  
 CC for determining if a test compound is a candidate compound for binding to  
 CC CD11b or for creating an inflammatory disorder, by contacting a test  
 CC compound with the polypeptide and determining if the test compound binds  
 CC to the polypeptide. The integrin subunits are useful for reducing  
 CC skeletal muscle injury, for treating disorders caused by ischaemia-  
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,  
 CC to purify variant integrin polypeptide ligands and as bait proteins in  
 CC two-hybrid or three-hybrid assays. This sequence represents a human  
 CC integrin alpha subunit CD11b variant A domain. Note: This variant  
 CC sequence is not featured in the specification but has been derived from  
 CC the wild-type protein shown in AAU76847

CC Sequence 191 AA:

Query Match 98.8%; Score 964; DB 5; Length 191;  
 Best Local Similarity 98.4%; Pred. No. 6,8e-98;  
 Matches 188; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTILFSIMQSEEFRIHFTFK 60  
 DB 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTILFSIMQSEEFRIHFTFK 60

QY 61 EFQNNPNPRSLVKPTITQLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120  
 DB 61 EFQNNPNPRSLVKPTITQLGRTHTATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120

QY 121 DPLGYEDVIPADREGVIRVYIGVDAPFRSEKSRQELNTIASKPRDHVFOVNNFEALKT 180  
 DB 121 DPLGYEDVIPADREGVIRVYIGVDAPFRSEKSRQELNTIASKPRDHVFOVNNFEALKT 180

QY 181 IONQLREKXFA 191  
 DB 181 IONQLREKXFA 191

QY 181 IONQLREKXFA 191  
 DB 181 IONQLREKXFA 191

QY 181 IONQLREKXFA 191  
 DB 181 IONQLREKXFA 191

QY 181 IONQLREKXFA 191  
 DB 181 IONQLREKXFA 191

QY 181 IONQLREKXFA 191  
 DB 181 IONQLREKXFA 191

QY 181 IONQLREKXFA 191  
 DB 181 IONQLREKXFA 191

RESULT 13  
 AAU76847  
 ID AAU76847 standard; protein; 191 AA.

AC AAU76847;



XX 21-MAY-2002 (first entry)  
 XX  
 DE Human integrin alpha subunit CD11b A domain.  
 XX  
 KW Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;  
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;  
 KW ischemia-reperfusion injury; immune complex; parasitic disease;  
 KW antinflammatory; vasotropic; antiparasitic; vulnery; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..188  
 FT /note="This region is specifically claimed"  
 XX  
 PN WO200209737-A1.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 31-JUL-2001; 2001WO-US023957.  
 XX  
 PR 31-JUL-2000; 2000US-0221950P.  
 PR 11-JAN-2001; 2001US-00758493.  
 PR 13-MAR-2001; 2001US-00805354.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 PI Arnaut AM, Li R, Xiong J;  
 DR WPI; 2002-188687/24.  
 XX  
 PT Novel high affinity integrin polypeptide useful for treating restenosis  
 PT and parasitic diseases, comprises all or part of variant integrin alpha  
 PT subunit A domain or variant integrin beta subunit A-like domain.  
 XX  
 PS Example 2; Fig 5; 55pp; English.  
 XX  
 CC The invention relates to a high affinity integrin polypeptide comprising  
 CC all or part of a variant integrin alpha subunit A domain or a variant  
 CC integrin beta subunit A-like domain. The polypeptide, preferably the  
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by  
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or  
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful  
 CC for determining if a test compound is a candidate compound for binding to  
 CC CD11b or for treating an inflammatory disorder, by contacting a test  
 CC compound with the polypeptide and determining if the test compound binds  
 CC to the polypeptide. The integrin subunits are useful for reducing  
 CC skeletal muscle injury, for treating disorders caused by ischemia-  
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,  
 CC to purify variant integrin polypeptide ligands and as bait proteins in  
 CC two-hybrid or three-hybrid assays. This sequence represents the human  
 CC integrin alpha subunit CD11b A domain  
 CC  
 XX  
 SQ Sequence 191 AA:  
 Query Match 98.8%; Score 964; DB 5; Length 191;  
 Best Local Similarity 97.9%; Pred. No. 6.8e-98;  
 Matches 187; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CPOEDSDIAFLIDSGSIIPHDPRMKFVSTWMEQLKSKTFLSLQYSEEFRIHFTFK 60  
 DB 1 CPOEDSDIAFLIDSGSIIPHDPRMKFVSTWMEQLKSKTFLSLQYSEEFRIHFTFK 60  
 QY 61 EFQNNPNPRLSVKPTQLGRTHTATGIRKVVRELFNTNGARKNAFLLVINDGEKFG 120  
 DB 61 EFQNNPNPRLSVKPTQLGRTHTATGIRKVVRELFNTNGARKNAFLLVINDGEKFG 120  
 QY 121 DPLGVEDVTPADREGVIRYVIGVDAPRSEKSEKROELNTIASKPPRDHVPQNNFEALKT 180  
 DB 121 DPLGVEDVTPADREGVIRYVIGVDAPRSEKSEKROELNTIASKPPRDHVPQNNFEALKT 180  
 QY 181 IQNQLREKXFA 191

DB 181 IQNQLREKXFA 191  
 RESULT 14  
 ID AAY21991 standard; protein; 187 AA.  
 AC AAY21991;  
 AC AAY21991;  
 DT 13-SEP-1999 (first entry)  
 XX  
 DE Human complement factor MAC-1 vWF domain sequence.  
 XX  
 KW Factor B analogue; modified; complement activity; complement factor B;  
 KW short consensus repeat domain; von Willebrand Factor domain; human; C2;  
 KW CR3; autoimmune response; tissue damage; lupus erythematosus; therapy;  
 KW rheumatoid arthritis; hemolytic anemia; myasthenia gravis; injury; MAC-1;  
 KW myocardial infarction; acute shock lung syndrome; inflammation; vWF.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5928892-A.  
 XX  
 PD 27-JUL-1999.  
 XX  
 PF 26-JUL-1996; 96US-00687706.  
 XX  
 PR 03-JAN-1994; 94US-00177109.  
 XX  
 PA (UNITV ) UNITV WASHINGTON.  
 PI Oglesby TJ, Hourcade DE;  
 DR WPI; 1999-429498/36.  
 XX  
 PT Nucleic acids encoding complement protein homologues useful for  
 PT modulating function of the complement system in the treatment of a  
 PT variety of immune and autoimmune complex mediated syndromes.  
 XX  
 PS Disclosure; Fig 5A-B; 53pp; English.  
 XX  
 CC The invention relates to a Factor B analogue that exhibits modified  
 CC complement activity in vitro. The analogue is generated by substituting a  
 CC short consensus repeat domain (SCR) or a von Willebrand Factor domain  
 CC (WVF) of human factor B with a SCR or a WVF from a second protein such as  
 CC human C2 or CR3. The analogues may be used to regulate the complement  
 CC system involved in immune and autoimmune responses. Complement activity  
 CC can account for substantial tissue damage in a wide variety of autoimmune  
 CC /immune complex mediated syndromes such as lupus erythematosus,  
 CC rheumatoid arthritis, hemolytic anemia and myasthenia gravis. Inhibition  
 CC of the complement system using the analogues is likely to provide a means  
 CC of therapeutic intervention in these cases. Inhibition of complement may  
 CC also be favorable in cases that involve tissue damage caused by vascular  
 CC injury such as myocardial infarction, cerebral vascular accidents or  
 CC acute shock lung syndrome. In these cases the complement system may  
 CC contribute to the destruction of partially damaged tissue as in  
 CC reperfusion injury. In addition, the use of complement analogues with  
 CC novel target specificities could reduce the activity of tissue damaging  
 CC proteins at sites of inflammation. Complement inhibition is important in  
 CC the prevention of xenograft rejection (the inhibition of complement by  
 CC cell-associated and soluble inhibitors is useful in protecting the  
 CC transplant from damage caused by activation of endogenous complement. The  
 CC present sequence represents the vWF domain of human factor MAC-1  
 CC  
 XX  
 SQ Sequence 187 AA:  
 Query Match 98.4%; Score 960; DB 2; Length 187;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-97;  
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CPOEDSDIAFLIDSGSIIPHDPRMKFVSTWMEQLKSKTFLSLQYSEEFRIHFTFK 60

Db 1 CPQEDSDIAFLINGSGSIIPHDPRRMEFVSTVMEQIKKSKTLPSLMQYSEEPRIHFTPK 60  
QY 61 EFQNNPNPSLVKPIITQLGRTHTATGIRKRVRELFNITNGARKNAFKILVITTDKFKG 120  
Db 61 EFQNNPNPSLVKPIITQLGRTHTATGIRKRVRELFNITNGARKNAFKILVITTDKFKG 120  
QY 121 DPLGYEDVPEADREGVIRYVIGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
Db 121 DPLGYEDVPEADREGVIRYVIGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
QY 181 IQNQLRE 187  
Db 181 IQNQLRE 187

## RESULT 15

AAB66766  
ID AAB66766 standard; protein; 216 AA.

XX AAB66766;

DT 10-APR-2001 (first entry)

DE Amino acids 149-353 of human CR-3 alpha chain and His tag.

KW EST, expressed sequence tag; inclusion body; binding partner;  
immunoglobulins.

OS Homo sapiens.  
OS Synthetic.

PN WO200102588-A2.

XX 11-JAN-2001.

PF 30-JUN-2000; 2000WO-EP006137.

FR 02-JUL-1999; 99EP-00112815.

PA (MORP-) MORPHOSYS AG.

PI Friesch C, Kretzschmar T, Hoess A, Von Rueden T;

DR WPI; 2001-147085/15.

PT Generating specific binding partners to (poly)peptides encoded by genomic  
DNA fragments, involves forming inclusion bodies by expressing the  
PT (poly)peptide as part of fusion proteins.

PS Disclosure; Page 18; 45pp; English.

XX The present invention relates to generating a specific binding partner to  
a peptide, encoded by a genomic DNA fragment or an expressed sequence tag  
CC (EST). A nucleic acid molecule encoding a fusion protein is expressed in  
CC a host cell to allow the formation of inclusion bodies comprising the  
CC fusion protein, the inclusion bodies are isolated and a specific binding  
CC partner is generated. The specific binding partners generated are useful  
CC for identifying and characterizing naturally occurring proteins e.g. as  
CC immunoglobulins or fragments in immunoassays

XX Sequence 216 AA;

Query Match 96.5%; Score 942; DB 4; Length 216;

Best Local Similarity 99.5%; Pred. No. 2.2e-95;  
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 SDIAFLINGSGSIIPHDPRRMEFVSTVMEQIKKSKTLPSLMQYSEEPRIHFTPK 65

Db 12 SDIAFLINGSGSIIPHDPRRMEFVSTVMEQIKKSKTLPSLMQYSEEPRIHFTPK 71

QY 66 PNPSLVKPIITQLGRTHTATGIRKRVRELFNITNGARKNAFKILVITTDKFKG 125

Db 72 PNPSLVKPIITQLGRTHTATGIRKRVRELFNITNGARKNAFKILVITTDKFKG 131

QY 126 EDVPEADREGVIRYVIGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 185  
Db 132 EDVPEADREGVIRYVIGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 191  
QY 186 REKIFA 191  
Db 192 REKIFA 197

Search completed: November 8, 2005, 21:22:31  
Job time : 168 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2005, 20:42:47 ; Search time 39 Seconds  
(without alignments)  
471.215 Million cell updates/sec

Title: US-09-805-354-1

Perfect score: 976

Sequence: 1 PQEDSDIAFLIDSGSIIP.....VNNFEALNTQNLREKKFA 191

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	974	99.8	1153	1	RMHUB		cell surface glyco
2	754	77.3	1153	1	S00551		leukocyte surface
3	548	56.1	1153	1	RMHUB		cell surface glyco
4	328	33.6	1179	2	A53213		integrin alpha-E c
5	288.5	29.6	1170	2	S03308		cell surface glyco
6	266	27.3	1163	2	I56126		lymphocyte function
7	241	24.7	493	2	A33809		cartilage matrix p
8	234	24.0	500	2	S66522		cartilage matrix p
9	231	23.7	466	2	A37929		cartilage matrix p
10	215.5	22.1	1151	2	A45226		integrin alpha-1 c
11	215	22.0	3124	2	A40020		collagen alpha 1(X
12	214.5	22.0	1747	2	A45974		collagen alpha 1(X
13	214.5	22.0	1857	2	S31212		collagen alpha 1(X
14	214.5	22.0	1888	2	S78476		collagen alpha 1(X
15	206.5	21.2	3051	2	A42373		hypothetical prote
16	205.5	21.1	272	2	A55348		integrin alpha-1 c
17	200.5	20.5	1180	2	A35854		integrin alpha-1 c
18	191.5	19.6	741	2	T46488		hypothetical prote
19	187	19.2	929	2	I51027		type XII collagen
20	174.5	17.9	2944	2	A54849		collagen alpha 1(V
21	163	16.7	3176	2	CGHUA		collagen alpha 3(V
22	162	16.3	3137	2	A37797		collagen alpha 3(V
23	159	16.3	1170	2	I45914		integrin alpha 2 c
24	154	15.8	1178	2	A33998		integrin alpha-2 c
25	154	15.0	1178	2	S44142		VLA-2 protein homo
26	146	14.7	550	2	T23760		hypothetical prote
27	143	14.4	371	2	A40970		undulin 1 - human
28	140.5	14.4	371	2	S32604		collagen alpha 2(V
29	135.5	13.9	763	2	I50807		complement factor

30	134.5	13.8	712	2	A45638		immunodominant mic
31	132	13.5	2813	1	VWHT		von Willebrand fac
32	130.5	12.9	191	2	I47230		VLA-2 protein - p1
33	125.5	12.9	1029	1	S21369		collagen alpha 2(V
34	124.5	12.8	1022	2	S04111		collagen alpha 2(V
35	122.5	12.6	238	2	C35243		collagen alpha 2(V
36	122.5	12.6	917	2	S09646		collagen alpha 2(V
37	122.5	12.6	1018	1	CGHUA		collagen alpha 2(V
38	119.5	12.2	724	2	A48569		antigen Em100 - B1
39	118.5	12.1	918	2	S23377		collagen alpha 2(V
40	117.5	12.0	1019	1	A32856		collagen alpha 1(V
41	115.5	11.8	427	2	G00039		von Willebrand fac
42	113.5	11.6	414	2	PS0323		complement factor
43	111	11.4	764	1	BRHU		hypothetical prote
44	109.5	11.2	567	2	T28797		hypothetical prote
45	109.5	11.2	13055	2	T16580		hypothetical prote

#### ALIGNMENTS

RESULT 1  
RMHUB  
cell surface glycoprotein CD11b precursor [validated] - human  
N:Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Ma  
eukocyte integrin alpha chain; neutrophil adherence receptor alphas chain  
C:Species: Homo sapiens (man)  
C>Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #ext change 09-Jul-2004  
C:Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567  
R:Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.  
J. Biol. Chem. 263, 12403-12411, 1988  
A>Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CR  
B.  
A:Reference number: A31108; MUID:88315033; PMID:2457584  
A:Accession: A31108  
A:Molecule type: mRNA  
A:Residues: 1-1153 <COR>  
A:Cross-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIND:AAA59544.1; PID:g30714  
A>Note: part of this sequence was confirmed by protein sequencing  
R:Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.  
J. Cell Biol. 106, 2153-2158, 1988  
A>Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor ;  
A:Reference number: A28915; MUID:88257215; PMID:2454931  
A:Accession: A28915  
A:Molecule type: mRNA  
A:Residues: 1-499, 501-965, 'P', 967-1153 <ARN>  
A:Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIND:AAA59  
A>Note: the authors translated the codon TAG for residue 1129 as Thr  
R:Shelley, C.S.; Arnaout, M.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991  
A>Title: The promoter of the CD11b gene directs myeloid-specific and developmentally re  
A:Reference number: A41600; MUID:92073318; PMID:1683702  
A:Accession: A41600  
A:Molecule type: DNA  
A:Residues: 1-9 <SHR>  
A:Cross-references: GB:M76724; NID:g180018; PIND:AAA5410.1; PID:g553215  
R:Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.  
Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988  
A>Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhes  
A:Reference number: A94193; MUID:88190151; PMID:2833753  
A:Accession: A30892  
A:Molecule type: mRNA  
A:Residues: 917-1042 <AR2>  
A:Cross-references: GB:M18044  
R:Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Beck, A.L.; Roth, G.J.  
Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989  
A>Title: cDNA sequence for the alpha subunit of the human neutrophil adherence recepto  
A:Reference number: A32218; MUID:8908893; PMID:2563162  
A:Accession: A32218  
A:Molecule type: mRNA  
A:Residues: 9-1153 <HC>  
A:Cross-references: GB:J04145; NID:g189068; PIND:AAA59903.1; PID:g386975

A>Note: part of this sequence was confirmed by protein sequencing  
R.Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.  
J.Immunol. 150, 480-490, 1993  
A>Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in  
n during evolution.  
A:Reference number: A46526; MUID:93123748; PMID:8419480  
A:Accession: A46526  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-499,501-1153 <FEb>  
A:Cross-references: GB:SS2227; NID:9263047; PIDN:AA824821.1; PID:9263049  
A>Note: the last three bases of intron 13, CAG, are included in some but not all mature  
A:Note: sequence extracted from NCBI backbone (NCBI:121963)  
R.Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.  
Biochim. Biophys. Acta 874, 368-371, 1986  
A>Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp  
A:Reference number: A50664; MUID:87076671; PMID:3539202  
A:Accession: A26091  
A:Molecule type: protein  
A:Residues: 17-31 <PIb>  
A:Experimental source: granulocytes  
R.Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.  
Blood 79, 865-870, 1992  
A>Title: Characterization of the myeloid-specific CD11b promoter.  
A:Reference number: 152567; MUID:92144986; PMID:1346576  
A:Accession: 152567  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-9 <RbS>  
A:Cross-references: GB:M84477; NID:9180184; PIDN:AAA51960.1; PID:9553219  
C:Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1  
C:Genetics:  
A:Gene: GDB:ITGAM; CR3A  
A:Cross-references: GDB:120599; OMIM:120980  
A:Map position: 16p11.2-16p11.2  
A>Note: promoter contains a GATA motif and two Sp1 consensus binding sites  
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom  
C:Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAt>  
F:17-1108/Domain: extracellular #status predicted <EXT>  
F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>  
F:465-473/Region: calcium/magnesium binding #status predicted  
F:530-538/Region: calcium/magnesium binding #status predicted  
F:593-601/Region: calcium/magnesium binding #status predicted  
F:1109-1134/Domain: transmembrane #status predicted <TMW>  
F:1153-1153/Domain: intracellular #status predicted <INT>  
F:86,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding  
Query Match 99.8%; Score 974; DB 1; Length 1153;  
Best Local Similarity 99.5%; Pred. No. 2,1e-75;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CPQEDSDIAFLIDSGSIIIPDPRMKEFVSTVMEQLKSKTFLSLMYSEEFRIHFTFK 60  
Db 144 CPQEDSDIAFLIDSGSIIIPDPRMKEFVSTVMEQLKSKTFLSLMYSEEFRIHFTFK 203  
Qy 61 EFQNNPNRSLVKPTQLGRTHTATGTRKVRRELPHNTNGARKNAFILLVITDGEKFG 120  
Db 204 EFQNNPNRSLVKPTQLGRTHTATGTRKVRRELPHNTNGARKNAFILLVITDGEKFG 263  
Qy 121 DPLGVEDVTPADREGVIRYVIGVDAFRSEKSRQELNTISKPRDHFVQVNNFEALKT 180  
Db 264 DPLGVEDVTPADREGVIRYVIGVDAFRSEKSRQELNTISKPRDHFVQVNNFEALKT 323  
Qy 181 IONQLREKXFA 191  
Db 324 IONQLREKXFA 334  
RESULT 2  
S00551  
leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse

N:Alternate names: complement-3 receptor alpha chain  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: S00551; 159078  
R.Pyela, R.  
EMBO J. 7, 1371-1378, 1988  
A>Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the i  
A:Reference number: S00551; MUID:88312584; PMID:3044779  
A:Accession: S00551  
A:Molecule type: DNA  
A:Residues: 1-1153 <PYT>  
A:Cross-references: UNIPROT:P05555; EMBL:X07640; NID:952982; PIDN:CAA30479.1; PID:952983  
A>Note: the authors translated the codon CAC for residue 569 as Gln  
R.Sastre, L.; Roman, J.M.; Teplov, D.B.; Dreyer, W.J.; Gee, C.B.; Larson, R.S.; Roberts,  
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986  
A>Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recep  
A:Reference number: 159078; MUID:86287312; PMID:2942940  
A:Accession: 159078  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 11-44 <RbS>  
A:Cross-references: GB:M4293; NID:9198993; PIDN:AAA9484.1; PID:9554193  
C:Genetics:  
A:Gene: Mac-1  
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo  
C:Keywords: cell adhesion; glycoprotein; transmembrane protein  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental  
F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>  
F:1106-1129/Domain: transmembrane #status predicted <TMW>  
Query Match 77.3%; Score 754; DB 2; Length 1153;  
Best Local Similarity 78.0%; Pred. No. 1.6e-56;  
Matches 149; Conservative 19; Mismatches 23; Indels 0; Gaps 0;  
Qy 1 CPQEDSDIAFLIDSGSIIIPDPRMKEFVSTVMEQLKSKTFLSLMYSEEFRIHFTFK 60  
Db 144 CPQEDSDIAFLIDSGSIIIPDPRMKEFVSTVMEQLKSKTFLSLMYSEEFRIHFTFK 203  
Qy 61 EFQNNPNRSLVKPTQLGRTHTATGTRKVRRELPHNTNGARKNAFILLVITDGEKFG 120  
Db 204 DFKNPNRSHVSPKQLNGRTKASGTRKVRRELPHNTNGARKNAFILLVITDGEKFG 263  
Qy 121 DPLGVEDVTPADREGVIRYVIGVDAFRSEKSRQELNTISKPRDHFVQVNNFEALKT 180  
Db 264 DPLGVEDVTPADREGVIRYVIGVDAFRSEKSRQELNTISKPRDHFVQVNNFEALKT 323  
Qy 181 IONQLREKXFA 191  
Db 324 IONQLREKXFA 334  
RESULT 3  
RWHUIC  
cell surface glycoprotein CD11c precursor - human  
N:Alternate names: leukocyte adhesion receptor p150,95 alpha chain  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004  
C:Accession: A36584; A35433; S00864  
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.  
J. Biol. Chem. 265, 12750-12751, 1990  
A:Reference number: A36584  
A:Contents: erratum  
A:Accession: A36584  
A:Molecule type: DNA  
A:Residues: 1-1163 <COR>  
A:Cross-references: UNIPROT:P20702  
A>Note: this revision to the sequence from reference A3543 includes the carboxyl end  
R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.  
J. Biol. Chem. 265, 2782-2788, 1990  
A>Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.  
A:Reference number: A3543; MUID:90153906; PMID:2303426  
A:Accession: A3543

A:Molecule type: DNA  
A:Residues: 1-834 <CO2>  
A>Note: This sequence has been revised in reference A36584  
R:Cordt, A.L.; Miller, L.O.; O'Connor, K.; Larson, R.S.; Springer, T.A.  
EMBO J. 6, 4023-4028, 1987  
A>Title: CDNA cloning and complete primary structure of the alpha subunit of a leukocyte  
A:Reference number: S00864; MUID:8816645; PMID:3327687  
A:Accession: S00864  
A:Molecule type: mRNA  
A:Residues: 1-755, V, 757-1163 <CO3>  
A:Cross-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830  
A>Note: Part of this sequence was confirmed by protein sequencing  
C:Comment: A common beta chain, (CD18) forms a heterodimer with CD11b to form Mac-1 on my  
C:Genetics:  
A:Gene: GDB:ITGAX; CD11C  
A:Cross-references: GDB:119758; OMIM:151510  
A:Map position: 16p11.2-16p11.2  
C:Superfamily: Cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom  
C:Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>  
F:20-1107/Domain: extracellular #status predicted <EXT>  
F:149-319/Domain: von Willebrand factor type A repeat homology <VWA4>  
F:1108-1133/Domain: transmembrane #status predicted <TM>  
F:1134-1163/Domain: intracellular #status predicted <INT>  
F:61,89,392,697,735,899,933,1050/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match                      56.1%; Score 548; DB 1; Length 1163;  
Best Local Similarity 56.0%; Pred. No. 7.5e-39;  
Matches 107; Conservative 34; Mismatches 50; Indels 0; Gaps 0;

OY    1 CQEDSDIAFLINGSGSIHDPFRMKEFVSTWNEQLKKSKTLPSLMOYSEBRIHPFK 60  
     ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db    145 CPQEQDIDYELDIGSGSISRRNFATMMFNFAVAVISQFPSPSTQSLPNSKFOTHFTFE 204  
  
OY    61 EPQNENPNRLVKPIPTQLKRTHTATGIRKVARELFNTTNGARKAKAFILVVITDGEXPG 120  
     ||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db    205 EFRTTSNPULSLASVHOLQGFYTITAIQNVYHLFHLSYGARRPATILIVITDGCKEG 264  
  
OY    121 DPLGVEDVIPADREGVIRYVIGVDAPFRSEKSQELNTIASKPRPDHFQVNNFEALKT 180  
     ||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db    265 DSLDYDVIPMAADAIGIRRAVGGLAFQNNRSWMKLNDIASKPQEHIKFVEDFDALKD 324  
  
OY    181 IQNLREKKAFA 191  
     ||::||::||  
Db    325 IQNLKEKIFA 335  
  
RESULT 4  
A53213  
Integrin alpha-E chain - human  
C:Species: Homo sapiens (man)  
C>Date: 19-Oct-1995 #sequence\_revision 31-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: A53213  
R:Shaw, S.K.; Cepke, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.  
J. Biol. Chem. 269, 6016-6025, 1994  
A>Title: Molecular cloning of the human mucosal lymphocyte integrin alpha(E) subunit. U  
A:Reference number: A53213; MUID:94164962; PMID:8119947  
A:Accession: A53213  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1179 <SHA>  
A:Cross-references: UNIPROT:P38570; GB:L25851; NID:g457244; PID:g457245  
C:Genetics:  
A:Gene: GDB:ITGAE  
A:Cross-references: GDB:330801  
A:Map position: 17p13  
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom  
F:199-771/Domain: von Willebrand factor type A repeat homology <VWA3>

Query Match                      33.6%; Score 328; DB 2; Length 1179;  
Best Local Similarity 38.8%; Pred. No. 5.7e-20;  
Matches 71; Conservative 42; Mismatches 68; Indels 2; Gaps 1;

QY 6 SDIAFLIDSGSIIIPHDFRMKFEVSTVWEQL--KSKSLTFLSMQYSEERIHFTKEPQ 63

Db 201 TEIAIILIDSGSIDPPDPFORAKDPISNMKNFEYKECECNFALVQGVQIOTEPDLRDSQ 260

QY 64 NNENPNSIVKPIITQOLGRHTTATGIRKVRBELFNINNGARKNAFKILVITIDSEKFGDPL 123

Db 261 DNASIAFVQNIITQVGSVTKTASAMQHVLDISITSSHGRSKRSKVMVVLTDGIFEDPL 320

QY 124 GYEDVPEADREAGVIRVIVGDAFPRSEKSRQELNTIASKPPRDHVFQVNNFEALKTION 183

Db 321 NLTVINSPPKQGVVERFALGVGEFPKSARFARRELNIASDPDETHAFKVTNNYALDGLLS 380

QY 184 QLR 186

Db 381 KLR 383

RESULT 5

S03308

cell surface glycoprotein CD11a precursor - human

N:Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function

C:Species: Homo sapiens (man)

C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004

C:Accession: S03308; A47458; A47565; A48759; S36044

R:R Larson, R.S.; Corbi, A.L.; Berman, L.; Springer, T.

J: Cell Biol. 108, 703-712, 1989

A:Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit

A:Reference number: S03308; MUID:89139587; PMID:2557322

A:Accession: S03308

A:Molecule type: mRNA

A:Residues: 1-1170 <L>R>

A:Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:g31421; PIDN:CAA68

A>Note: part of this sequence was confirmed by protein sequencing

R:Corneill, R.D.; Gollan, K.A.; Hickstein, D.D.

Proc. Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993

A:Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) pr

A:Reference number: A47458; MUID:93248261; PMID:8097887

A:Accession: A47458

A:Molecule type: DNA

A:Residues: 1-20 <COR>

A>Note: sequence extracted from NCBI backbone (NCBIN:130862, NCBI:P:130863)

R:Shelley, C.S.; Farokhzad, O.C.; Arnaout, M.A.

Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993

A:Title: Identification of cell-specific and developmentally regulated nuclear factors

A:Reference number: A47565; MUID:93281759; PMID:8099450

A:Accession: A47565

A:Molecule type: DNA

A:Residues: 1-20 <SHB>

A:Cross-references: GB:M95609

R:Nuada, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.

J. Biol. Chem. 268, 19305-19311, 1993

A:Title: Characterization of the CD11a (alphaL, LFA-1alpha) integrin gene promoter.

A:Reference number: A48759; MUID:93374910; PMID:8103515

A:Accession: A48759

A:Molecule type: DNA

A:Residues: 1-20 <NHE>

A:Cross-references: EMBL:Z22804; NID:g311405; PIDN:CAA80461.1; PID:g311406

C:Genetics:

A:Gene: GDB:ITGAL; CD11A

A:Cross-references: GDB:119757; OMIM:153370

A:Map position: 16p11.2-16p11.2

C:Superfamily: cell surface glycoprotein CD1b; von Willebrand factor type A repeat hom

C:Keywords: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface antigen; tr

F.1-25/Domains: signal sequence #status predicted <SIG>

F.126-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted

F.154-317/Domains: von Willebrand factor type A repeat homology <VWA>

Query Match 29.6%; Score 288.5; DB 2; Length 1170;

Best Local Similarity 32.6%; Fred. No. 1.4e-16;

Matches 62; Conservative 50; Mismatches 71; Indels 7; Gaps 2;

1 CPQEDSDIAFLIDSGSIIIPHDFRMKFEVSTVWEQLKSKSLTFLSMQYSEERIHFTKEP 60

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Db      150 CTKGNVDLVFLFDGSGMSIQPDFQKILDFMKQVMKKLSNTSYQFAAVQFSTSYKTEPDFS 209
Qy      61 EFQNNPNRSLVLPKPTQLGLGRTHTATGIRKVVRELFNITNGARKNAFKILVITTGKFG 120
Db      210 DYVKMKDVPDLKHKHMLLNTGALNYVATEVFRRELGRPRATVLLITDGE--A 267
Qy      121 DPLGEDVYIPADREGVIRYVGVGDAPRSEKSRQELNTIASKPRPDHVPQVNNFEALKT 180
Db      268 TDSGNIDAKD-----IIRYIIGIKKHQTKESQGLTKHKFASKPASEFVKILDTTEKLD 322
Qy      181 IQNQLRECKF 190
Db      323 LFTLELQKKIY 332

```

## RESULT 6

```

156126 lymphocyte fuction-associated molecule-1-alpha - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: 156126
R:Kaufmann, Y.; Teeng, E.; Springer, T.A.
J. Immunol. 147, 369-374, 1991
A:Title: Cloning of the murine lymphocyte fuction-associated molecule-1 alpha-subunit a
A:Reference number: 156126; MUID:91268576; PMID:2051027
A:Accession: 156126
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1163 <RES>
A:Cross-references: UNIPROT:P24063; GB:M60778; NID:G198785; PID:AAA39426.1; PID:G198786
C:Genetics:
A:Gene: LFA-1
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol
P:151-315/Domain: von Willebrand factor type A repeat homology <VMA1>

```

```

Query Match      27.3%; Score 266; DB 2; Length 1163;
Best Local Similarity 32.2%; Pred. No. 1.2e-14;
Matches 64; Conservative 40; Mismatches 73; Indels 22; Gaps 3;

```

```

Qy      1 CPQESDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTLPSLMQYSEEFRIHFFPK 60
Db      147 CMKGKVDLVFLFDGSGMSIQPDFQKILDFMKQVMKKLSNTSYQFAAVQFSTDCRTEPFL 206
Qy      61 EF-QNNPNRSLVLPKPTQLGLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGK 119
Db      207 DYVKMKDVPDLKHKHMLLNTGALNYVATEVFRRELGRPRATVLLITDGE--A 263
Qy      120 GDLPEDEVIPADREG-----VIRYVGVGDAPRSEKSRQELNTIASKPRPDHVPQV 172
Db      264 -----EASDKGNISAAHDITRYIIGIKHFKFVSQKQTLHIFASEPVEEFVKIL 312
Qy      173 NNFEALKTIQNQLRECKFA 191
Db      313 DTFEKLDLFTDLQRIYA 331

```

## RESULT 7

```

A33809 cartilage matrix protein precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C:Accession: A33809; A26364
R:Klas, I.; Deak, F.; Hollway Jr., R.G.; Delius, H.; Meubst, K.A.; Frimberger, E.; Argz
J. Biol. Chem. 264, 8126-8134, 1989
A:Title: Structure of the gene for cartilage matrix protein, a modular protein of the ex
grins, von Willebrand factor, complement factors B and C2, and epidermal growth factor.
A:Reference number: A33809; MUID:89255246; PMID:2542265
A:Accession: A33809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-493 <KTS>
A:Cross-references: UNIPROT:P05099; GB:X12346; GB:X12347; GB:X12348; GB:X12349; GB:X1235

```

```

R:Argaves, W.S.; Deak, F.; Sparkes, K.J.; Kiehl, I.; Goectinck, P.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
A:Title: Structural features of cartilage matrix protein deduced from cDNA.
A:Reference number: A26364; MUID:87092429; PMID:3025875
A:Accession: A26364
A:Molecule type: mRNA
A:Residues: 78-493 <ARG>
A:Cross-references: GB:M4792; NID:G211545; PID:AAA48695.1; PID:G211546
C:Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
P:337-204/Domain: von Willebrand factor type A repeat homology <VMA1>
F:225-260/Domain: EGF homology <EGF>
F:270-434/Domain: von Willebrand factor type A repeat homology <VMA2>

```

```

Query Match      24.7%; Score 241; DB 2; Length 493;
Best Local Similarity 31.4%; Pred. No. 5.6e-13;
Matches 59; Conservative 38; Mismatches 73; Indels 18; Gaps 4;

```

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Qy      7 DIAFLIDSGSGIIPHDFRMKEFVSTVMEQLKKS--KTLPSLMQYSEEFRIHFFKEFQ 64
Db      272 DLVFLIDSGSKVRENFEVLVKFINGIVESLESEKQAVGLVQSSVRQEPFLGQPKN 331
Qy      65 NPNRSLVLPKPTQLGLGRTHTATGIRKVVRELFNITNGARKNAFKILVITTGKFGDPLG 124
Db      332 KKDIAKAVKXKAVMEKGMTGQALKLYVDSFSIANGARPGVPVGIPTDGRS----- 385
Qy      125 YEDVIPADRE---GVIRYVGVGDAPRSEKSRQELNTIASKPRPDHVPQVNNFEALKT 180
Db      386 -QDYITDAKAKAKDLGRMPAVGVGNV-----EDLEIREIASEVVAHEHYFTADPRTISN 439
Qy      181 IQNQLREK 188
Db      440 IGRKLQWK 447

```

## RESULT 8

```

S66522 cartilage matrix protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66522
R:Aszodi, A.; Hauser, N.; Stueder, D.; Paulsach, M.; Hirtl, L.; Bosze, Z.
Eur. J. Biochem. 236, 970-977, 1996
A:Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein c
A:Reference number: S66522; MUID:96270751; PMID:8665920
A:Accession: S66522
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-500 <ASZ>
A:Cross-references: UNIPROT:P51942; EMBL:U35035; NID:G1163178; PID:AA06521.1; PID:G116
C:Genetics:
A:Gene: CMP
C:Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-500/Product: cartilage matrix protein #status predicted <MAT>
F:43-210/Domain: von Willebrand factor type A repeat homology <VMA1>
F:231-266/Domain: EGF homology <EGF>
F:277-441/Domain: von Willebrand factor type A repeat homology <VMA2>

```

```

Query Match      24.0%; Score 234; DB 2; Length 500;
Best Local Similarity 29.6%; Pred. No. 2.3e-12;
Matches 56; Conservative 44; Mismatches 71; Indels 18; Gaps 4;

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Qy      6 SDIAFLIDSGSGIIPHDFRMKEFVSTVMEQLKSKTL--FSLMQYSEEFRIHFFKEFQ 63
Db      278 TDLVFLIDSGSKVRENFEVLVKFINGIVLDSRLAOGVLQVSSSRQEPFLGRFH 337
Qy      64 NPNRSLVLPKPTQLGLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGKFGDPL 123
Db      338 SKKDIAKAVNMVMEKGMTGQALKLYVDSFSIANGARPGVGVPTDGRS----- 392
Qy      124 GYEDVIPADRE---GVIRYVGVGDAPRSEKSRQELNTIASKPRPDHVPQVNNFEALK 179
Db      393 --QDYINDAKAKAKDLGRMPAVGVGNV-----EDELREIASEPVADHVFYTDAPFTIN 445

```



J Biol. Chem. 261, 17724-17727, 1987  
 A.Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin  
 A.Reference number: S22254; MUID:88087065; PMID:3121603  
 A.Accession: S22254  
 A.Molecule type: protein  
 A.Residues: 2831-2832, 'T', 2834, 'R', 2836-2843, 3002-3014 <DUB>  
 R.Trueb, J.; Trueb, B.  
 Biochim. Biophys. Acta 1171, 97-98, 1992  
 A.Title: The two splice variants of collagen XII share a common 5' end.  
 A.Reference number: S28811; MUID:93042014; PMID:1420368  
 A.Accession: S28811  
 A.Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-24, 1189-1257, 'S', 1259-1263, 'E', 1265-1280 <TRU>  
 A.Cross-references: EMBL:X67327  
 C.Genetics: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1  
 C.Keywords: alternative splicing; cell binding; coiled coil; connective tissue; disulfide  
 F.1-23/Domain: signal sequence #status predicted <SIG>  
 F.24-3124/Product: collagen alpha 1(XII) chain #status predicted <MNT>  
 F.24, 1189-3124/Product: collagen alpha 1(XII) chain short splice form #status predicted  
 F.24-114/Domain: I11A #status predicted <I11A>  
 F.24-105/Domain: fibronectin type III repeat homology <FN3A>  
 F.1137-301/Domain: von Willebrand factor type A repeat homology <VWA1>  
 F.333-425/Domain: I11B #status predicted <I11B>  
 F.333-414/Domain: fibronectin type III repeat homology <FN3B>  
 F.437-601/Domain: von Willebrand factor type A repeat homology <VWA2>  
 F.623-1178/Domain: I11C #status predicted <I11C>  
 F.430-711/Domain: fibronectin type III repeat homology <FN3C>  
 F.7721-802/Domain: fibronectin type III repeat homology <FN3D>  
 F.812-895/Domain: fibronectin type III repeat homology <FN3E>  
 F.995-986/Domain: fibronectin type III repeat homology <FN3F>  
 F.995-1076/Domain: fibronectin type III repeat homology <FN3G>  
 F.1086-1169/Domain: fibronectin type III repeat homology <FN3H>  
 F.1137-1361/Domain: von Willebrand factor type A repeat homology <VWA3>  
 F.1384-2295/Domain: I11D #status predicted <I11D>  
 F.1384-1465/Domain: fibronectin type III repeat homology <FN3I>  
 F.11474-1557/Domain: fibronectin type III repeat homology <FN3J>  
 F.1566-1647/Domain: fibronectin type III repeat homology <FN3K>  
 F.1655-1738/Domain: fibronectin type III repeat homology <FN3L>  
 F.1756-1838/Domain: fibronectin type III repeat homology <FN3M>  
 F.1847-1928/Domain: fibronectin type III repeat homology <FN3N>  
 F.1937-2019/Domain: fibronectin type III repeat homology <FN3O>  
 F.2028-2110/Domain: fibronectin type III repeat homology <FN3P>  
 F.2119-2199/Domain: fibronectin type III repeat homology <FN3Q>  
 F.2207-2294/Domain: fibronectin type III repeat homology <FN3R>  
 F.2355-2490/Domain: von Willebrand factor type A repeat homology <VWA4>  
 F.2438-2440/Domain: cell adhesion #status predicted  
 F.2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status predicted  
 F.2751-2902/Domain: collagenous COL2 #status predicted <COL2>  
 F.2899-2901/Region: cell attachment (R-G-D) motif  
 F.2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>  
 F.2946-3048/Domain: collagenous COL1 #status predicted <COL1>  
 F.3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>  
 F.32, 1006, 1032, 1044, 1512, 1767, 2210, 2273, 2532, 2683/Binding site: carbohydrate (Asn)  
 F.2780, 2789, 2836, 2842, 2860, 2869, 3004, 3007/Modified site: hydroxyproline (Pro) #stat

QY 180 TIONOL 185  
DB 306 DIONEI 311

RESULT 12  
A45974  
collagen alpha 1(XIV) chain precursor, short form 2 - chicken

N.Alternate names: undulin  
C.Species: Gallus gallus (chicken)  
C.Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C.Accession: A45974, S20085; S22916; S17035; S20833  
R.Geracke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin  
J. Biol. Chem. 268, 12177-12184, 1993  
A.Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region  
na.  
A.Reference number: A45974; MUID:93280195; PMID:8505337  
A.Accession: A45974

A.Status: preliminary  
A.Molecule type: mRNA, protein  
A.Residues: 1-1747 <GER>  
A.Cross-references: UNIPROT:P32018  
A.Experimental source: embryo skin  
A.Note: sequence inconsistent with the nucleotide translation  
A.Note: sequence extracted from NCBI backbone (NCBI:133364, NCBI:P133365)  
R.Appe, S.S.  
submitted to the EMBL Data Library, March 1992  
A.Reference number: S30085  
A.Accession: S30085  
A.Molecule type: mRNA  
A.Residues: 1472-1660 <APT>  
A.Cross-references: EMBL:X65122, NID:G62871, PIDN:CAA46238.1, PID:G938175  
R.Trueb, J.; Trueb, B.  
Eur. J. Biochem. 207, 549-557, 1992  
A.Title: Type XIV collagen is a variant of undulin.  
A.Reference number: S22916, MUID:92339443, PMID:1339349  
A.Accession: S22916  
A.Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 286-494, 'Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 <TRU>  
R.Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne,  
Eur. J. Biochem. 201, 333-338, 1991  
A.Title: Cloning of a cDNA for a new member of the class of fibrin-associated collagens  
A.Reference number: S17035, MUID:92037585, PMID:1935930  
A.Accession: S17035  
A.Molecule type: mRNA  
A.Residues: 1472-1659 <GOR1>  
A.Accession: S20833  
A.Molecule type: protein  
A.Residues: 1551-1570, 1593-1599, 1639-1667 <GOR2>  
C.Keywords: alternative splicing; coll'd coll; extracellular matrix; glycoprotein; trime  
P.40-204/Domain: von Willebrand factor type A repeat homology <VMA1>  
F.236-317/Domain: fibronectin type III repeat homology <FN3A>  
F.326-409/Domain: fibronectin type III repeat homology <FN3B>  
F.418-498/Domain: fibronectin type III repeat homology <FN3C>  
F.507-591/Domain: fibronectin type III repeat homology <FN3D>  
F.625-707/Domain: fibronectin type III repeat homology <FN3E>  
F.716-798/Domain: fibronectin type III repeat homology <FN3F>  
F.806-893/Domain: fibronectin type III repeat homology <FN3G>  
F.924-1089/Domain: von Willebrand factor type A repeat homology <VMA2>  
F.1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>  
F.1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>  
F.1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>

Query Match 22.0%; Score 214.5; DB 2; Length 1747;  
Best Local Similarity 32.4%; Pred. No. 5.1e-10;  
Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;

QY 1 CPOESDIAFLIDSGSIIIPHDFRMKEFV-STV--MEQKKSKTLFSLIMQYSEEFRIHF 57  
DB 920 CCAAKADLVFLVDGSHSIDGDNFNKIIISFLYSTVGALDKIGPDGTQVAIIIGESDDRIEF 979

58 TPKERQNNENPRLSVKPIQLGRHTATGIRKVRLEFNITNGARKNAFKILVITDGE 117



Db 980 KLNAYKTELTLEAIOQLAYKGNKTKKAIKHAREVFTGBAGRKGI PKVLVITDGR 1039  
Qy 118 KFGDPLGVEDVYPEADREGVIRYVGVGDAFSEKSRQELNTIASKPRPDHVOVNNFEA 177  
Db 1040 SODD---VNKVSREMQLDGFSFPAIGVADADYS-----ELVNIGSKPSEBRHVFVDDFDA 1091  
Qy 178 LKTIQNL 185  
Db 1092 FTKIEDEL 1099

RESULT 13  
S31212  
collagen alpha 1(XIV) chain precursor, short form - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 15-Sep-2003  
C:Accession: S31212  
R:Maclchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.  
E: J. Biochem. 212, 483-490, 1993  
A:Title: Complete primary structure of chicken collagen XIV.  
A:Reference number: S31211; MUID:93185668; PMID:844186  
A:Accession: S31212  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-1857 <MAE>  
A:Cross-references: EMBL:X70792; NID:9288874; PIDN:CA50063.1; PID:9288875  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993  
C:Genetics:  
A:Gene: COL14A1  
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>  
F:29-110/Domain: fibronectin type III repeat homology <FN3A>  
F:29-320/Domain: von Willebrand factor type A repeat homology <VWA1>  
F:352-433/Domain: fibronectin type III repeat homology <FN3B>  
F:442-525/Domain: fibronectin type III repeat homology <FN3C>  
F:534-614/Domain: fibronectin type III repeat homology <FN3D>  
F:623-707/Domain: fibronectin type III repeat homology <FN3E>  
F:741-823/Domain: fibronectin type III repeat homology <FN3F>  
F:832-914/Domain: fibronectin type III repeat homology <FN3G>  
F:922-1009/Domain: fibronectin type III repeat homology <FN3H>  
F:1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 22.0%; Score 214.5; DB 2; Length 1857;  
Best Local Similarity 32.4%; Pred. No. 5.5e-10;  
Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;

Db 1036 CAAKADLVFLVDGWSIGDDNFNKIISFLYVGVGALDKIGPDGVOVALIQSDDPRTF 1095  
Qy 58 TFEKQNNPNRSLVKPITQLGRTHTATGIRKVVRELNTNGARKNAFKILVITDGE 117  
Db 1096 KLNAYKTELTLEAIOQLAYKGNKTKKAIKHAREVFTGBAGRKGI PKVLVITDGR 1155  
Qy 118 KFGDPLGVEDVYPEADREGVIRYVGVGDAFSEKSRQELNTIASKPRPDHVOVNNFEA 177  
Db 1156 SODD---VNKVSREMQLDGFSFPAIGVADADYS-----ELVNIGSKPSEBRHVFVDDFDA 1207  
Qy 178 LKTIQNL 185  
Db 1208 FTKIEDEL 1215

RESULT 14  
S78476  
collagen alpha 1(XIV) chain precursor, long form - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 09-Jul-2004  
C:Accession: S78476; S31211  
R:Trueb, B.  
submitted to the EMBL Data Library, January 1993

A:Reference number: S78476  
A:Accession: S78476  
A:Molecule type: mRNA  
A:Residues: 1-1888 <TRU>  
A:Cross-references: UNIPROT:P32018; EMBL:X70793; NID:9288872; PIDN:CA50064.1; PID:92888  
R:Maclchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.  
E: J. Biochem. 212, 483-490, 1993  
A:Title: Complete primary structure of chicken collagen XIV.  
A:Reference number: S31211; MUID:93185668; PMID:844186  
A:Accession: S31211  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1416;1460-1811,1843-1888 <MAE>  
A:Cross-references: EMBL:X70793  
C:Genetics:  
A:Gene: COL14A1  
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>  
F:29-110/Domain: fibronectin type III repeat homology <FN3A>  
F:29-320/Domain: von Willebrand factor type A repeat homology <VWA1>  
F:352-433/Domain: fibronectin type III repeat homology <FN3B>  
F:442-525/Domain: fibronectin type III repeat homology <FN3C>  
F:534-614/Domain: fibronectin type III repeat homology <FN3D>  
F:623-707/Domain: fibronectin type III repeat homology <FN3E>  
F:741-823/Domain: fibronectin type III repeat homology <FN3F>  
F:832-914/Domain: fibronectin type III repeat homology <FN3G>  
F:922-1009/Domain: fibronectin type III repeat homology <FN3H>  
F:1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 22.0%; Score 214.5; DB 2; Length 1888;  
Best Local Similarity 32.4%; Pred. No. 5.6e-10;  
Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;

Db 1036 CAAKADLVFLVDGWSIGDDNFNKIISFLYVGVGALDKIGPDGVOVALIQSDDPRTF 1095  
Qy 58 TFEKQNNPNRSLVKPITQLGRTHTATGIRKVVRELNTNGARKNAFKILVITDGE 117  
Db 1096 KLNAYKTELTLEAIOQLAYKGNKTKKAIKHAREVFTGBAGRKGI PKVLVITDGR 1155  
Qy 118 KFGDPLGVEDVYPEADREGVIRYVGVGDAFSEKSRQELNTIASKPRPDHVOVNNFEA 177  
Db 1156 SODD---VNKVSREMQLDGFSFPAIGVADADYS-----ELVNIGSKPSEBRHVFVDDFDA 1207  
Qy 178 LKTIQNL 185  
Db 1208 FTKIEDEL 1215

RESULT 15  
S42373  
hypothetical protein T7065.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 07-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-May-2004  
C:Accession: S42373  
R:Smith, A.  
submitted to the EMBL Data Library, March 1994  
A:Reference number: S42368  
A:Accession: S42373  
A:Molecule type: DNA  
A:Residues: 1-3051 <SMI>  
A:Cross-references: EMBL:Z30423; NID:9458479; PID:9458485  
C:Genetics:  
A:Intron: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;  
F:512-679/Domain: von Willebrand factor type A repeat homology <VWA1>  
F:754-793/Domain: fibronectin type II repeat homology <2F1>  
F:1201-1244/Domain: EGF homology <EGF>

Query Match 21.2%; Score 206.5; DB 2; Length 3051;  
Best Local Similarity 31.7%; Pred. No. 5e-09;  
Matches 63; Conservative 40; Mismatches 71; Indels 25; Gaps 8;



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: November 8, 2005, 20:47:13 ; Search time 177 Seconds  
(without alignments)  
552.583 Million cell updates/sec

Title: US-09-805-354-1  
Perfect score: 976  
Sequence: 1 CPQEDSDIAFLIDSGSIIP.....VNFEALKTIONQLREKXFA 191

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974	99.8	1152	ITAM_HUMAN	P11215 homo sapien
2	787	80.6	920	Q28984	Q28984 sus scrofa
3	754	77.3	1153	ITAM_MOUSE	P05555 mus musculus
4	727	74.5	1151	Q9J130	Q9J130 ratu
5	609	62.4	205	Q63001	Q63001 ratu
6	603	61.8	1161	ITAD_RAT	Q9QY67 ratu
7	591	60.6	1162	ITAD_HUMAN	Q13349 homo sapien
8	548	56.1	1163	ITAX_HUMAN	P20702 homo sapien
9	542	55.5	1188	Q6KAS4	Q6KAS4 mus musculus
10	541	55.4	1169	ITAX_MOUSE	Q9QXK4 mus musculus
11	408	41.8	304	Q6PG66	Q6PG66 mus musculus
12	343	35.1	895	Q9WUF8	Q9WUF8 mus sp. Itg
13	343	35.1	1167	Q8B340	Q8B340 ratu
14	341	34.9	1038	Q8BS01	Q8BS01 mus musculus
15	337	34.5	1167	ITAE_MOUSE	Q60677 mus musculus
16	328	33.6	1179	ITAE_HUMAN	P38570 homo sapien
17	326	33.0	1160	Q8MKF4	Q8MKF4 felis silve
18	322.5	33.0	1167	Q8B341	Q8B341 ratu
19	319	30.9	231	Q8N882	Q8N882 homo sapien
20	302	30.7	79	Q8HY27	Q8HY27 ovis aries
21	302	30.9	79	Q8HY41	Q8HY41 bos taurus
22	292.5	30.0	1170	ITAI_HUMAN	P20701 homo sapien
23	285.5	29.3	1165	ITAI_BOVIN	P61625 bos taurus
24	280	28.7	269	Q80WE9	Q80WE9 ratu
25	266	27.3	1160	Q9R200	Q9R200 mus musculus
26	266	27.3	1161	Q9WTV4	Q9WTV4 mus musculus
27	265.5	27.2	1163	ITAI_MOUSE	P24063 mus musculus
28	261.5	26.8	1166	Q6TYB8	Q6TYB8 bos taurus
29	251.5	25.8	1187	Q98TF0	Q98TF0 cyprinus ca
31	247	25.3	257	Q8C270	Q8C270 mus musculus

32	241	24.7	493	1	CAMA_CHICK	P05099 gallus gall
33	237	24.3	652	2	Q9SLI2	Q9SLI2 bos taurus
34	234	24.0	500	1	CAMA_MOUSE	P51942 mus musculus
35	234	24.0	500	2	Q80VNS	Q80VNS mus musculus
36	231	23.7	496	1	CAMA_HUMAN	P21941 homo sapien
37	231	23.7	656	2	Q96DT1	Q96DT1 homo sapien
38	231	23.7	678	2	Q9UDN0	Q9UDN0 homo sapien
39	231	23.7	693	2	Q96DM8	Q96DM8 homo sapien
40	226.5	23.2	1086	2	Q96HB1	Q96HB1 homo sapien
41	222.5	22.8	589	2	Q7ZX63	Q7ZX63 xenopus lae
42	222.5	22.8	755	2	Q00261	Q00261 homo sapien
43	222.5	22.8	956	2	Q99K64	Q99K64 mus musculus
44	221	22.6	650	2	Q8VH15	Q8VH15 mus musculus
45	220.5	22.6	915	2	Q6UMAS	Q6UMAS homo sapien

## ALIGNMENTS

RESULT 1  
ITAM\_HUMAN STANDARD; PRT; 1152 AA.  
ID ITAM\_HUMAN  
AC P11215;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (leukocyte adhesion receptor) (Neutrophil adherence receptor).  
DE (Neutrophil adherence receptor).  
GN Name=ITGAM; Synonyms=CD11B, CR3A;  
OS Homo sapiens (Human).  
OC Chordata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88315033; PubMed=2457584;  
RA Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;  
RT "The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B.";  
RT J. Biol. Chem. 263:12403-12411(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=883190151; PubMed=2833753;  
RA Arnaut M.A., Remold-O'Donnell E., Pierre M.W., Harris P., Tenen D.G.;  
RT "Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mo1: chromosomal localization and homology to the alpha subunits of integrins.";  
RT Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88257215; PubMed=2454931; DOI=10.1083/jcb.106.6.2153;  
RA Arnaut M.A., Gupta S.K., Pierce M.W., Tenen D.G.;  
RT "Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mo1 (complement receptor type 3).";  
RT J. Cell Biol. 106:2153-2158(1988).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9313748; PubMed=8419480;  
RA Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.P., Tenen D.G.;  
RT "Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during evolution.";  
RT J. Immunol. 150:480-490(1993).  
RN [5]  
RP SEQUENCE OF 9-1153 FROM N.A.  
RX MEDLINE=89098893; PubMed=2563162;  
RA Hickey D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L., Roth G.J.;  
RT "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).  
RN [6]  
RN SEQUENCE OF 1-9 FROM N.A.  
RX MEDLINE=92073318; PubMed=1683702;  
RA Shelley C.S., Arnaut M.A.;  
RT "The promoter of the CD11b gene directs myeloid-specific and  
RT developmentally regulated expression.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).  
RN [7]  
RN SEQUENCE OF 1-9 FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=92144986; PubMed=1346576;  
RA Pahl H.L., Rosemarin A.G., Tenen D.G.;  
RT "Characterization of the myeloid-specific CD11b promoter.";  
RL Blood 79:865-870(1992).  
RN [8]  
RN SEQUENCE OF 17-31.  
RX MEDLINE=87076671; PubMed=3539202; DOI=10.1016/0167-4838(86)90037-3;  
RA Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaut M.A.;  
RT "N-terminal sequence of human leukocyte glycoprotein Mol: conservation  
RT across species and homology to platelet Iib/Iita.";  
RL Biochim. Biophys. Acta 874:368-371(1986).  
RN [9]  
RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.  
RX MEDLINE=95171458; PubMed=7867070; DOI=10.1016/S0969-2126(95)90517-0;  
RA Lee J.O., Rieu P., Arnaut M.A., Liddington R.;  
RT "Crystal structure of the A domain from the alpha subunit of integrin  
RT CR3 (CD11b/CD18)." ;  
RL Cell 80:631-638(1995).  
RN [10]  
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.  
RX MEDLINE=96363671; PubMed=8747460; DOI=10.1016/S0969-2126(01)00271-4;  
RA Lee J.O., Bankston L.A., Arnaut M.A., Liddington R.C.;  
RT "Two conformations of the integrin A-domain (I-domain): a pathway for  
RT activation?";  
RL Structure 3:1333-1340(1995).  
RN [11]  
RN X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.  
RX MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;  
RA Baldwin E.T., Saver R.W., Bryant G.L., Curry K.A.,  
RA Faidbanks M.B., Finzel B.C., Garlick R.L., Heinrichson R.L.,  
RA Horton N.C., Kelley L.L., Milder A.M., Moon U.B., Mott J.E.,  
RA Mutchler V.T., Tomich C.S., Matempaugh K.D., Wiley V.H.;  
RT "Calcium binding to the integrin CD11b I domain and activation model  
RT assessment." ;  
RL Structure 6:923-935(1998).  
RN [12]  
RN 3D-STRUCTURE MODELING OF 17-616.  
RX MEDLINE=9826734; PubMed=9560195; DOI=10.1073/pnas.95.9.4870;  
RA Oxyvig C., Springer T.A.;  
RT "Experimental support for a beta-propeller domain in integrin alpha-  
RT subunits and a calcium binding site on its lower surface.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).  
RN [1]  
RN FUNCTION: Integrin alpha-M/beta-2 is implicated in various  
RN adhesive interactions of monocytes, macrophages and granulocytes  
RN as well as in mediating the uptake of complement-coated particles.  
RN It is identical with CR-3, the receptor for the ICB fragment of  
RN the third complement component. It probably recognizes the R-G-D  
RN peptide in Cdb. Integrin alpha-M/beta-2 is also a receptor for  
RN fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides  
RN of fibrinogen gamma chain.  
RN [2]  
RN SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M  
RN associates with beta-2.  
RN [3]  
RN SUBCELLULAR LOCATION: Type I membrane protein.  
RN [4]  
RN TISSUE SPECIFICITY: Predominantly expressed in monocytes and  
RN granulocytes.  
RN [5]  
RN DOMAIN: The integrin I-domain (insert) is a VMPA domain. Integrins  
RN with I-domains do not undergo protease cleavage.  
RN [6]  
RN SIMILARITY: Belongs to the integrin alpha chain family.  
RN [7]  
RN SIMILARITY: Contains 7 FG-GAP repeats.  
RN [8]  
RN SIMILARITY: Contains 1 VMPA domain.  
RN [9]  
RN DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;  
RN WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".

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CC -----  
DR EMBL; J03925; AAA59544.1; -;  
DR EMBL; M18044; AAA59491.1; -;  
DR EMBL; J04145; AAA59903.1; -;  
DR EMBL; S52227; AAB24821.1; -;  
DR EMBL; S52152; AAB24821.1; JOINED.  
DR EMBL; S52153; AAB24821.1; JOINED.  
DR EMBL; S52154; AAB24821.1; JOINED.  
DR EMBL; S52155; AAB24821.1; JOINED.  
DR EMBL; S52157; AAB24821.1; JOINED.  
DR EMBL; S52159; AAB24821.1; JOINED.  
DR EMBL; S52161; AAB24821.1; JOINED.  
DR EMBL; S52164; AAB24821.1; JOINED.  
DR EMBL; S52165; AAB24821.1; JOINED.  
DR EMBL; S52167; AAB24821.1; JOINED.  
DR EMBL; S52169; AAB24821.1; JOINED.  
DR EMBL; S52170; AAB24821.1; JOINED.  
DR EMBL; S52173; AAB24821.1; JOINED.  
DR EMBL; S52174; AAB24821.1; JOINED.  
DR EMBL; S52180; AAB24821.1; JOINED.  
DR EMBL; S52181; AAB24821.1; JOINED.  
DR EMBL; S52184; AAB24821.1; JOINED.  
DR EMBL; S52189; AAB24821.1; JOINED.  
DR EMBL; S52191; AAB24821.1; JOINED.  
DR EMBL; S52192; AAB24821.1; JOINED.  
DR EMBL; S52203; AAB24821.1; JOINED.  
DR EMBL; S52212; AAB24821.1; JOINED.  
DR EMBL; S52213; AAB24821.1; JOINED.  
DR EMBL; S52216; AAB24821.1; JOINED.  
DR EMBL; S52219; AAB24821.1; JOINED.  
DR EMBL; S52220; AAB24821.1; JOINED.  
DR EMBL; S52221; AAB24821.1; JOINED.  
DR EMBL; S52222; AAB24821.1; JOINED.  
DR EMBL; S52226; AAB24821.1; JOINED.  
DR EMBL; M76724; AAA58410.1; -;  
DR EMBL; M84477; AAA51960.1; -;  
DR PIR; A31108; RMWH1B.  
DR PDB; 1A8X; Model; @=17-1152.  
DR PDB; 1BHO; X-ray; 1/2=-.  
DR PDB; 1BHQ; X-ray; 1/2=-.  
DR PDB; 1IDN; X-ray; 1/2=-.  
DR PDB; 1IDO; X-ray; @=140-331.  
DR PDB; 1JLM; X-ray; @=143-334.  
DR PDB; 1MIU; X-ray; A=137-331.  
DR PDB; 1MF7; X-ray; A=144-337.  
DR PDB; 1N9Z; X-ray; A=140-335.  
DR PDB; 1NA5; X-ray; A=144-345.  
DR Genew; HGNC:6149; ITGAM.  
DR MIM; 120980; -;  
DR GO; GO:0008305; C:integrin complex; TAS.  
DR GO; GO:0007155; P:cell adhesion; TAS.  
DR InterPro; IPR000413; Integrin\_alpha.  
DR Pfam; PF00357; Integrin\_alpha; 1.  
DR Pfam; PF00092; VWA; 1.  
DR PRINTS; PRO1185; INTEGRIN.  
DR PRINTS; PRO0453; WFPADOMAIN.  
DR SMART; SM00191; Int\_alpha; 5.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
DR PROSITE; PS50234; VMPA; 1.  
DR 3D-structure; Calcium; Cell adhesion; Direct protein sequencing;  
DR Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;  
DR Transmembrane.

FT	SIGNAL	1	16	Integrin alpha-M.
FT	CHAIN	17	1152	
	Query Match		99.8%;	Score 974; DB 1; Length 1152;
	Best Local Similarity		99.5%;	Pred. No. 1,1e-70;
	Matches 190;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
Qy	1 CPQEDSDIAFLIDSGSIIIPHDPRRMKEFVSTWMEQLKSKTILPSLMQYSEEFRIHPTFK	60		
Db	144 CPQEDSDIAFLIDSGSIIIPHDPRRMKEFVSTWMEQLKSKTILPSLMQYSEEFRIHPTFK	203		
Qy	61 EFQNNPNRSILVKPTQLLGRTHATGIRKVVRELFNTNGARKKAFILVITDGKEFG	120		
Db	204 EFQNNPNRSILVKPTQLLGRTHATGIRKVVRELFNTNGARKKAFILVITDGKEFG	263		
Qy	121 DPLGVEDYIPPADRGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFOVNFALKT	180		
Db	264 DPLGVEDYIPPADRGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFOVNFALKT	323		
Qy	181 IONOLREKXFA 191			
Db	324 IONOLREKXFA 334			
	RESULT 2			
ID	Q28984	PRELIMINARY;	PRT;	920 AA.
AC	Q28984;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	CD11b (Fragment) .			
GN	Name=CD11b;			
OS	Sus scrofa (Pig) .			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
NCBI_TaxId=9823;				
	[1]			
RP	SEQUENCE FROM N.A.			
RV	Lee J.-K., Schook L.B., Rutherford M.S.;			
RL	Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity) .			
CC	-1- SIMILARITY: Belongs to the Integrin alpha chain family.			
DR	EMBL; U40072; AAB16869.1; -.			
DR	HSP; P11215; INA5.			
DR	GO: GO:0016021; C:integral to membrane; IEA.			
DR	GO: GO:0008305; C:protein complex; IEA.			
DR	GO: GO:0005515; F:protein binding; IEA.			
DR	GO: GO:0007160; P:cell-matrix adhesion; IEA.			
DR	GO: GO:0007229; P:integrin-mediated signaling pathway; IEA.			
DR	InterPro: IPR000413; Integrin_alpha.			
DR	InterPro: IPR02035; VWF_A.			
DR	Pfam: PF00092; VWA_1.			
DR	PRINTS: PRO185; INTEGRIN.			
DR	SMART: SM00453; VWFADOMAIN.			
DR	SMART: SM00191; Int_alpha; 4.			
DR	SMART: SM00327; VWA_1.			
DR	PROSITE: PSS0234; VWF_A; 1.			
KW	Cell adhesion; Integrin; Transmembrane.			
FT	NON_TER	1		
FT	NON_TER	1		
FT	SEQUENCE	920 AA;	102440 MW;	E96CC51B350DD5AC CRC64;
	Query Match		80.6%;	Score 787; DB 2; Length 920;
	Best Local Similarity		80.6%;	Pred. No. 1.5e-55;
	Matches 154;	Conservative	18;	Mismatches 19; Indels 0; Gaps 0
Qy	1 CPQEDSDIAFLIDSGSIIIPHDPRRMKEFVSTWMEQLKSKTILPSLMQYSEEFRIHPTFK	60		
Db	11 CPQEDSDIAFLIDSGSIIIPHDPRRMKEFVSTWMEQLKSKTILPSLMQYSEEFRIHPTFK	70		
Qy	61 EFQNNPNRSILVKPTQLLGRTHATGIRKVVRELFNTNGARKKAFILVITDGKEFG	120		
Db	11 EFQNNPNRSILVKPTQLLGRTHATGIRKVVRELFNTNGARKKAFILVITDGKEFG	120		

Db 71 DFKRNSPKLLVRPRLQLGRHTTATGIRKRVTRLEFHSKSGARENALKILVITDGEKFG 130

Qy 121 DPLGVEDVIEADREGVIRYVIGVDGDAFRSEKSRQELNTTASKEPPDHVQVNNFEALKT 160  
|||||  
Db 131 DPLGVEDVIEADREGVIRYVIGVDGDAFNSWKSREELNTTASKEGCHVFOVNNFEAVKT 190  
|||||

Qy 181 IONOLREKFA 191  
|||||  
Db 191 IONOLREKFA 201  
|||||

RESULT 3  
ITAM\_MOUSE STANDARD; PRT; 1153 AA.

AC ID ITAM\_MOUSE STANDARD; PRT; 1153 AA.  
AC AC 050555; O8CA73;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Integrin alpha-M precursor (Cell surface glycoprotein MHC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).  
GN Name:Itgam;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RN SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=88312584; PubMed=3044779;  
RA Pyrela R.;  
RT "Antico acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor."  
RL EMOB J. 7:1371-1378 (1988).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;  
RX MEDLINE=22354683; PubMed=12466851; DOI=i0.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikiroldi I., Osato N., Saito R., Suzuki H., Yamana K., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gajobori T., Baldaralli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriber L.M., Kenakin A., Matsuda H., Batciov S., Beisel K.W., Blake J.A., Bratt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragan T.A., Fletcher C.F., Forrester A., Frerz K.S., Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Guelcinich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L., Kanaga A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numa K., Okido T., Pavan W.J., Pereira G., Peele G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Raveisi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Saito A., Schneider C., Sempke C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Terasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watson J., Wells C., Wilming L.G., Wysshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
[3]  
RN SEQUENCE OF 11-45 FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Spleen;  
RX MEDLINE=86287312; PubMed=2942940;  
RA Sastre L., Roman J.M., Teplov D.B., Dreyer W.J., Gee C.E., Larson R.S., Roberts T.M., Springer T.A.;  
RT "A partial genomic DNA clone for the alpha subunit of the mouse

RT complement receptor type 3 and cellular adhesion molecule Mac-1.",  
RT Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).  
RN [4]  
RP SEQUENCE OF 17-28.  
RX MEDLINE=85188276; PubMed=3887182;  
RA Springer T.A., Teplow D.B., Dreyer W.J.;  
RT "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion  
RT glycoproteins and unexpected relation to leukocyte interferon."  
RL Nature 314:540-542(1985).  
CC -1- FUNCTION: Integrin alpha-M/beta-2 is implicated in various  
CC adhesive interactions of monocytes, macrophages and granulocytes  
CC as well as in mediating the uptake of complement-coated particles.  
CC It is identical with CR-3, the receptor for the iC3b fragment of  
CC the third complement component. It probably recognizes the R-G-D  
CC peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for  
CC fibrinogen, factor X and ICHM1. It recognizes P1 and P2 peptides  
CC of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in  
CC glomerulonephritis. Mice expressing a null mutation of the alpha-M  
CC subunit gene demonstrate increase in neutrophil accumulation, in  
CC response to a impaired degradation and phagocytosis, events that  
CC apparently accelerate apoptosis in neutrophils. These mice develop  
CC obesity.  
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M  
CC associates with beta-2.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=P05555-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=P05555-2; Sequence=VSP\_010473;  
CC Note=No experimental confirmation available;  
CC -1- TISSUE SPECIFICITY: Predominantly expressed in monocytes and  
CC granulocytes.  
CC -1- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins  
CC with I-domains do not undergo protease cleavage.  
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.  
CC -1- SIMILARITY: Contains 7 FG-GAP repeats.  
CC -1- SIMILARITY: Contains 1 VWFA domain.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X07640; CA30479.1; -.  
DR EMBL; AK039444; BAC30350.1; -.  
DR EMBL; M14293; AAA39484.1; -.  
DR PIR; S00551; S00551.  
DR HSSP; P11215; 1BHQ.  
DR MGD; MGI:96607; Itgam.  
DR GO; GO:0009897; C:external side of plasma membrane; IDA.  
DR GO; GO:0007155; P:cell adhesion; IMP.  
DR GO; GO:0045123; P:cellular extravasation; IMP.  
DR GO; GO:0030593; P:neutrophil chemotaxis; IMP.  
DR InterPro; IPR000413; Integrin\_alpha.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF01839; FG-GAP\_3-  
DR Pfam; PF00357; Integrin\_alpha; 1.  
DR Pfam; PF00092; VWA\_1  
DR PRINTS; PRO1185; INTEGRIN.  
DR PRINTS; PRO0453; WVFADOMAIN.  
DR SMART; SMO0327; VWA; 1.  
DR SMART; SMO0327; VWA; 1.  
DR PROSITE; PS00242; INTEGRIN\_ALPHA; 1.  
DR PROSITE; PS00234; VWFA\_1  
KW Alternative splicing; Calcium; Cell adhesion;  
KW Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;  
KW Signal; Transmembrane.

FT	SIGNAL	1	16	
FT	CHAIN	17	1153	Integrin alpha-M.
FT	DOMAIN	17	1105	Extracellular (Potential).
FT	TRANSMEM	1106	1129	Potential.
FT	DOMAIN	1130	1153	Cytoplasmic (Potential).
FT	REPEAT	31	84	FG-GAP 1.
FT	REPEAT	85	163	FG-GAP 2.
FT	DOMAIN	164	350	VWFA.
FT	REPEAT	337	400	FG-GAP 3.
FT	REPEAT	401	452	FG-GAP 4.
FT	REPEAT	454	515	FG-GAP 5.
FT	REPEAT	517	575	FG-GAP 6.
FT	REPEAT	580	632	FG-GAP 7.
FT	CA_BIND	465	473	Potential.
FT	CA_BIND	529	537	Potential.
FT	CA_BIND	592	600	Potential.
FT	SITE	1132	1136	GFFKR motif.
FT	DISULFID	66	73	By similarity.
FT	DISULFID	105	123	By similarity.
FT	DISULFID	654	711	By similarity.
FT	DISULFID	770	776	By similarity.
FT	DISULFID	999	1023	By similarity.
FT	DISULFID	1028	1033	By similarity.
FT	CARBOHYD	58	58	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	86	86	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	391	391	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	696	696	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	734	734	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	772	772	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	801	801	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	881	907	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	907	907	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	941	941	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	980	980	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	994	994	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1022	1022	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1045	1045	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1051	1051	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1076	1076	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	453	569	Missing (in isoform 2).
FT	CONFLICT	37	37	FTId=VSP_010473.
FT	CONFLICT	683	683	N -> S (in Ref. 2).
FT	CONFLICT	1153 AA;	127480 MW;	V -> G (in Ref. 2).
FT	SEQUENCE	1153 AA;	127480 MW;	178DB988AECB0343 CRC64;
SO	SEQUENCE	1153 AA;	127480 MW;	178DB988AECB0343 CRC64;
Query Match				
Best Local Similarity 77.3%; Score 754; DB 1; Length 1153;				
Matches 149; Conservative 19; Mismatches 23; Indels 0; Gaps 0;				
QY	1	CPQEDSDIAFLIDSGSITPHDFFRMKKEFVSIVMEQLKSKSTLFSIMQYSEFRIFHTFK	60	
DB	144	CPQESDVIPLIDSGSININIDFQMKKEFVSIVMEQFKSKSTLFSIMQYSDERIRIFHTN	203	
QY	61	EFQNNPNRSLVYPITQILGRTHATGIRKVVRELNTNGARKNAFKTLVITDGEKRG	120	
DB	204	DKRNPSPRSHVSPITQILNGRTKTASGIRKVVRELPHKTNGARENAKLIVITDDEKRG	263	
QY	121	DLGLGVEDVPEADREGVIRYVGVDAFPESEKSRQELNTASKEPPDHYFOVNNFEALKT	180	
DB	264	DLPLDYKDVPEADRGVIRYVGVGNFAFKPSRRELDTTASPAGEHVFOVNNFEALNT	323	
QY	181	IONOLREKKFA	191	
DB	324	IONOLREKKFA	334	
RESULT 4				
Q9U130	PRELIMINARY;	PRT;	1151 AA.	
AC	Q9U130;			
DT	01-OCT-2000 (TREMBlrel. 15, Created)			
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)			
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)			

```

DE Integrin beta 2 alpha subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Fathallah D.M. Sr., Zeria K. Jr.
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; AR268593; AAF81280.1; -.
DR HSSP; P11215; IBHQ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR004113; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VMA; 1.
DR PRINTS; PR01185; INTEGRIN.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VMA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS50234; VMPA; 1.
DR Cell adhesion; Integrin; Transmembrane.
KM
SQ SEQUENCE 1151 AA; 126943 MW; 8F785659D4074C45 CRC64;

Query Match 74.5%; Score 727; DB 2; Length 1151;
Best Local Similarity 74.3%; Pred. No. 1.5e-50;
Matches 142; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 1 CPOEDSIAFLIDSGSGIIPHDPRMKEFVSTWELQKSKTLFSLMOYSEEPRIHTFK 60
DB 144 CPOESNIAFLIDSGSINTIDFQKMEFVSTWDOFKSKTLFSLMOYSEEPRIHTFN 203
DB 61 EFONNPRLSVKRTQLGRTHATGIRKVRRELFTITGARGNAFKIIVITDGEKFG 120
DB 204 DFKNPDPKSHVRPIROLNGRTKTASGIRKVRRELFOKINGARNNAKILVITDGEKFG 263
QY 121 DPLGVDEVIDEADREGVIRVYIGVDAFRSEKSRQELNTIASKEPRDHVQVNNFEALKT 180
DB 264 DPLNVEVIDEADREGVIRVYIGVDAFRSEKSRQELNTIASKEPRDHVQVNNFEALNT 323
QY 181 IQNQLREKIFA 191
DB 324 IRNQLQEKIFA 334

RESULT 5
ID Q63001 PRELIMINARY; PRT; 205 AA.
AC Q63001;
DT 01-NOV-1996 (TREMURel. 01, Created)
DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
DT 01-JUN-2003 (TREMURel. 24, Last annotation update)
DE Integrin alpha-M (Fragment).
GN Name=Itgam;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Wistar Kyoto;
RA Nabika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier F.,
RA Julier C., Masuda J., Yamori Y., Nara Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59601; AAB03226.1; -.
DR HSSP; P11215; IBHQ.

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DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VMA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VMA; 1.
DR PROSITE; PS50234; VMPA; 1.
KM Integrin.
FT NON_TER 1
FT NON_TER 205
FT NON_TER 205
SQ SEQUENCE 205 AA; 22922 MW; C8C2D9395008DA36 CRC64;

Query Match 62.4%; Score 609; DB 2; Length 205;
Best Local Similarity 74.7%; Pred. No. 9e-42;
Matches 121; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 30 VSTWELQKSKTLFSLMOYSEEPRIHTFKPEFQNNPRLVKTPTQLGRTHATGIR 89
DB 1 VSTWELQKSKTLFSLMOYSEEPRIHTFKPEFQNNPRLVKTPTQLGRTHATGIR 60
QY 90 KTVRELFTITGARGNAFKIIVITDGEKRGDPLGVEDVPEADREGVIRVYIGVDAFR 149
DB 61 KTVRELFOKINGARNNAKILVITDGEKRGDPLGVEDVPEADREGVIRVYIGVDAFR 120
QY 150 SEKSRQELNTIASKEPRDHVQVNNFEALKTIONQLREKIFA 191
DB 121 KPOSRELDITASKPAGDHVQVNDPEALNTINQLQEKIFA 162

RESULT 6
ID ITND_RAT STANDARD; PRT; 1161 AA.
AC Q00YF;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor.
GN Name=Itgad;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley;
RA O'Brien M.M., VanderVlieten M., Kilgannon P.D., Dietrich G.,
RA Gallatin W.M.;
RL "Cloning of rat alpha D, a novel beta 2 integrin.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
CC VCAM1. May play a role in the atherosclerotic process such as
CC clearing lipoproteins from plaques and in phagocytosis of blood-
CC borne pathogens, particulate matter, and senescent erythrocytes
CC from the blood (By similarity).
CC -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
CC associates with beta-2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- DOMAIN: The Integrin I-domain (insert) is a VWF domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -1- SIMILARITY: Belongs to the integrin alpha chain family.
CC -1- SIMILARITY: Contains 7 FG-GAP repeats.
CC -1- SIMILARITY: Contains 1 VWF domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC or send an email to license@sib-sb.ch.
CC -----
DR EMBL; AF021334; AAF21241.1; -.
DR HSSP; P11215; IBHQ.
DR InterPro; IPR000413; Integrin_alpha.

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FT CA\_BIND 467 475 Potential.  
 FT CA\_BIND 531 539 Potential.  
 FT CA\_BIND 594 602 Potential.  
 FT SITE 1140 1144 GPRK motif.  
 FT DISULFID 69 76 By similarity.  
 FT DISULFID 108 126 By similarity.  
 FT DISULFID 656 711 By similarity.  
 FT DISULFID 770 776 By similarity.  
 FT DISULFID 858 873 By similarity.  
 FT DISULFID 1007 1031 By similarity.  
 FT DISULFID 1036 1041 By similarity.  
 FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 267 267 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 734 734 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 949 949 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 1059 1059 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 1084 1084 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 1169 AA; 129150 MW; C616412033C219A6 CRC64;

Query Match 55.4%; Score 541; DB 1; Length 1169;  
 Best Local Similarity 55.0%; Pred. No. 2.3e-35;  
 Matches 105; Conservative 32; Mismatches 54; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTK 60  
 DB 146 CPKQDDIVFLIDSGSISSTDFEKLDFVKAWMSQLQRPSTRFSLMPSDYFRVHFTN 205  
 QY 61 EFQNNPNPSLVKPTIQLGRTHTATGIRKVRBELNITNGARKNAFKLIVTTDSEKRG 120  
 DB 206 NFISTSSPLSLGVSQRLRGYVTASAIKRVITELFTTOSGARQDXTKVLIVTTDRKOG 265  
 QY 121 DPLGYEDVPEADREGVIRYVIGVGDAPFSEKRSKROELNTASKPRPDHYFOVNNPEALT 180  
 DB 266 DNLSTDSVTPMAEASIIIRYALGVGKAFYNEHSKQELKALIASPSHEHYVFSVENFDALD 325  
 QY 181 IONQLREKXFA 191  
 DB 326 IENQLKEKIFA 336

RESULT 11  
 ID Q6PG66 PRELIMINARY; PRT; 304 AA.  
 AC Q6PG66;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Integrin alpha X.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCBITaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;  
 RX MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Hoptkin S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E., Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.I., Wang J., Gay L.J., Hultyk S.W., Villalón D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;  
 RA Strausberg R.;  
 RL Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.  
 DR EMBL, BC057200; AAH57200.1; -  
 DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.  
 DR InterPro; IP002035; VWF\_A.  
 DR Pfam; PF00092; VWF\_1.  
 DR PRINTS; PR00453; VWFADOMAIN.  
 DR SMART; SM00327; VWF; 1.  
 DR PROSITE; PS50234; VWF; 1.  
 KW Integrin.  
 SQ SEQUENCE 304 AA; 33404 MW; EC52F3EAA8FA068D CRC64;

Query Match 41.8%; Score 408; DB 2; Length 304;  
 Best Local Similarity 53.3%; Pred. No. 3.5e-25;  
 Matches 80; Conservative 25; Mismatches 43; Indels 2; Gaps 1;

QY 1 CPQEDSDIAFLIDSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTK 60  
 DB 146 CPKQDDIVFLIDSGSISSTDFEKLDFVKAWMSQLQRPSTRFSLMPSDYFRVHFTN 205  
 QY 61 EFQNNPNPSLVKPTIQLGRTHTATGIRKVRBELNITNGARKNAFKLIVTTDSEKRG 120  
 DB 206 NFISTSSPLSLGVSQRLRGYVTASAIKRVITELFTTOSGARQDXTKVLIVTTDRKOG 265  
 QY 121 DPLGYEDVPEADREGVIRYVIGVGDAPFSEKRSKROELNTASKPRPDHYFOVNNPEALT 180  
 DB 266 DNLSTDSVTPMAEASIIIRYALGVGKAFYNEHSKQELKALIASPSHEHYVFSVENFDALD 325

RESULT 12  
 ID Q9WUP8 PRELIMINARY; PRT; 895 AA.  
 AC Q9WUP8;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DE Itgae protein (Fragment).  
 GN Name=Itgae;  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCBITaxID=10095;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Schoen M.P., Arya A., Murphy E.A., Adams C.M., Strauch U.G., Agace W.W., Marval J., Donohue J.P., Her H., Beier D.R., Olson S., LeFrancis L., Brenner M.B., Grusby M.J., Parker C.M.;  
 RL Submitted (Mar-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 DR EMBL, AF133085; AAD30063.1; JOINED.  
 DR EMBL, AF133070; AAD30063.1; JOINED.  
 DR EMBL, AF133071; AAD30063.1; JOINED.  
 DR EMBL, AF133072; AAD30063.1; JOINED.  
 DR EMBL, AF133073; AAD30063.1; JOINED.  
 DR EMBL, AF133074; AAD30063.1; JOINED.  
 DR EMBL, AF133075; AAD30063.1; JOINED.  
 DR EMBL, AF133076; AAD30063.1; JOINED.  
 DR EMBL, AF133077; AAD30063.1; JOINED.  
 DR EMBL, AF133078; AAD30063.1; JOINED.  
 DR EMBL, AF133079; AAD30063.1; JOINED.  
 DR EMBL, AF133080; AAD30063.1; JOINED.  
 DR EMBL, AF133081; AAD30063.1; JOINED.  
 DR EMBL, AF133082; AAD30063.1; JOINED.  
 DR EMBL, AF133083; AAD30063.1; JOINED.  
 DR EMBL, AF133084; AAD30063.1; JOINED.

	DR	HSSP; P11215; IBHQ.	
	DR	GO; GO:0016021; C:integral to membrane; IEA.	
	DR	GO; GO:0008305; C:integrin complex; IEA.	
	DR	GO; GO:0005515; F:protein binding; IEA.	
	DR	GO; GO:0007160; E:cell-matrix adhesion; IEA.	
	DR	GO; GO:0007229; E:integrin-mediated signalling pathway; IEA.	
	DR	InterPro; IPR000413; Integrin_alpha.	
	DR	InterPro; IPR002035; VWF_A.	
	Pfam; PF00092; VWA; 1.		
	KW	Cell adhesion; Integrin; Transmembrane.	
	FT	NON_TER	NON_TER
	SQ	SEQUENCE	BEEBA1AA754DADE CRC64;
			895 AA; 98265 MW; BECEA1AA754DADE CRC64;
			Query Match
			Best Local Similarity 35.1%; Score 343; DB 2; Length 895;
			Matches 71; Conservative 46; Mismatches 69; Indels 2; Gaps 14;
Oy	3	QEDSDIAFLIDSGSIIIPDFRNMKEFYSTNWOL--KSKTLFSLMOYSEEFRIHFEX	60
Dd	178	EGETIATVLDGGSIEPSDPFKAKNFISTMRNFEKCFCBCFNALVOIGAVITGFBLQ	237
Oy	61	FRONNPNRPISLVKPPTQLLGRTHTAGIRKVRELFNTNGARKNAFILVVITDGKERFG	120
Dd	238	BERDINASLAKVQSIVQEVTIKTMSAMQHVLDNFIFSRGSRKKALKMNVLTGDJIFG	297
Oy	121	DLGVGEDVIPEADREGVIRYYVGVDAPFERSEKSROLINTIASKPPRDHVFQVNFAELKT	180
Dd	298	DELNIATTVINSPKMGGVVRFAIGVGAFKNMTVELKLADIADPKEAHTFKVTNSALDG	357
Oy	181	IIONLRXK 188	
Dd	358	LUSLKQR 365	
* RESULT 13			
ID	088340	PRELIMINARY; PR1; 1167 AA.	
AC	088340,		
DT	01-NOV-1998 (TrEMBLrel_08, Created)		
DT	01-NOV-1998 (TrEMBLrel_08, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel_26, last annotation update)		
DE	Integrin alpha E1.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
NCBI_Taxid=10116;	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98056820; PubMed=9394838;		
RA	Brenan W., Rees D.J.G.;		
RT	"Sequence analysis of rat integrin alpha E1 and alpha E2 subunits:		
RT	tissue expression reveals phenotypic similarities between		
RL	epithelial lymphocytes and dendritic cells in lymph."		
CC	- SUBCELLULAR LOCATION: Type I transmembrane protein (By similarity).		
CC	- SIMILARITY: Belongs to the integrin alpha chain family.		
DR	EMBL; AF020045; AAC23662.1; -		
DR	HSSP; P11215; IBHQ.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0008305; C:integrin complex; IEA.		
DR	GO; GO:0005515; F:protein binding; IEA.		
DR	GO; GO:0007160; E:cell-matrix adhesion; IEA.		
DR	GO; GO:0007229; E:integrin-mediated signaling pathway; IEA.		
DR	InterPro; IPR000413; Integrin_alpha.		
DR	InterPro; IPR002035; VWF_A.		
DR	Pfam; PF00037; Integrin_alpha; 1.		
DR	Pfam; PF00092; VWA; 1.		

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DR PRINTS; PR001185; INTEGRINA.
DR PRINTS; PR00453; VMPADOMAIN.
DR SMART; SM00191; Int_alpha; 4.
DR SMART; SM00327; VMA_1 ALPHA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS50234; VMA; 1.
KW Cell adhesion; Integrin; Transmembrane.
KW Cell adhesion; Integrin; Transmembrane.
SQ SEQUENCE 1167 AA; 128969 MW; D88A2C38ACDC2AAB CRC64;

Query Match 35.1%; Score 343; DB 2; Length 1167;
Best Local Similarity 37.8%; Pred. No. 3.2e-19;
Matches 71; Conservative 46; Mismatches 69; Indels 2; Gaps 1;

QY 3 QEDSDIALINGSSSIIPHDRMKKEFSTVMEQL--KSKTLFLSMQYSEEPRIHFFFK 60
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 191 EDGEIATVLDGSGSIEPSDFOKAKNFTSTMRKRYEKCEFCNCALVQGVAVIQTEPDLQ 250
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 EFQNNPNFRSLVPKPTQLLGRTHATGIRKVRLEFNITNGARRNAEFKILVITDEKEFG 120
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 251 ESRDINMSLAKVQSIIVQKEVTKTASAMQHYLDNIFIPSRGSRKALKVMVVLTDGDIIFG 310
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 121 DPLGVEDVPEADREGVRRYVIGGDARFSEKSKQEOELNTIAKSPRQHPVQNNPEALKT 180
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 311 DPLNTTITVINSPPKQGVVRFPAIGVDAPKNNNTYRELKTLASDPEAHTFRTVYSALDG 370
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 181 IQNQLREK 188
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 371 LLSKLQQR 378

RESULT 14
Q8BS01 PRELIMINARY; PRT; 1038 AA.
ID Q8BS01;
AC Q8BS01;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length
   enriched library, clone:A530055U10 product:integrin, alpha E,
   epithelial-associated, full insert sequence.
DE Name:Itgae;
GN Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=99279953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation Of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA The FANTOM Consortium;
RT "The RIKEN genome Exploration Research Group Phase I & II Team;
   Analysis of the mouse transcriptome based on functional annotation of
   60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/9r.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
   Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

```



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FT REPEAT 566 631 FG-GAP 4.
FT REPEAT 634 686 FG-GAP 5.
FT CA_BIND 514 522 Potential.
FT CA_BIND 578 586 Potential.
FT CA_BIND 646 654 Potential.
FT DOMAIN 185 191 Glu-rich (acidic).
FT SITE 1140 1144 GFPK motif.
FT DISULFID 72 83 By similarity.
FT DISULFID 130 164 By similarity.
FT DISULFID 698 754 By similarity.
FT DISULFID 814 820 By similarity.
FT DISULFID 884 898 By similarity.
FT DISULFID 998 1023 By similarity.
FT DISULFID 1031 1047 By similarity.
FT CARBOHYD 51 51 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 314 314 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 341 341 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 364 364 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 418 418 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 437 437 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 718 718 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 773 773 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 829 829 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 846 846 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 911 911 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 925 925 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 968 968 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1013 1013 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1055 1055 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1086 1086 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1167 AA; 128983 MW; B8331C115DCCCFD CRC64;

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Query March 34.5%; Score 337; DB 1; Length 1167;

Best Local Similarity 37.2%; Pred. No. 9.8e-19; Matches 70; Conservative 46; Mismatches 70; Indels 2; Gaps 1;

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QY 3 QEDSDIAFLIDSGSIIIPDFRMKEFVSTVMEQL--KSKTLFSLMQYSEEFRIHFTFK 60
Db 191 EDGTEIATVLDGSGISGSDQKAKNFISTWNRNFYEKCECNFALVQYGAIVQTEFDLQ 250
QY 61 EFQNNPNSRLVAKPTQLGRTHTATGIRKVRBELFNITNGARKNAFKILVITDSEKFG 120
Db 251 ESRDINASLAKVQGIIVQKEVTKTASAMQHLDNIFLPSRGSRRKALKWVLTGDI FG 310
QY 121 DPLGYEDVTPADREGVRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 311 DPLNLTVTINSFKMGVRFALGVGDRFKNNNTYRELKLINSDPREAHTFKVTNYSALDG 370
QY 181 IQNQLREK 188
Db 371 LSKLQQR 378

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Search completed: November 8., 2005, 21:26:17  
Job time : 179 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2005, 21:12:18 ; Search time 42 Seconds  
(without alignments)  
339.476 Million cell updates/sec

Title: US-09-805-354-1

Perfect score: 976  
Sequence: 1 CPQEDSDIAFLIDSGSGSIIP.....VNNFALKTIONQLREKXFA 191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCtUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974	99.8	1152	2	US-08-476-062A-43
2	974	99.8	1152	5	PCT-US96-01314-43
3	974	99.8	1152	6	5424399-2
4	974	99.8	1152	1	US-08-173-497-3
5	974	99.8	1153	1	US-08-286-889-3
6	974	99.8	1153	1	US-08-485-618-3
7	974	99.8	1153	1	US-08-362-652-3
8	974	99.8	1153	1	US-08-605-672-3
9	974	99.8	1153	2	US-08-482-293A-3
10	974	99.8	1153	2	US-08-943-363-3
11	974	99.8	1153	3	US-09-193-043-3
12	974	99.8	1153	4	US-09-688-307A-3
13	974	99.8	1153	4	US-09-350-259-3
14	974	99.8	1153	4	US-09-688-307A-3
15	960	98.4	187	2	US-08-177-109A-61
16	960	98.4	187	2	US-08-687-706-61
17	942	96.5	216	4	US-09-795-872-5
18	942	96.5	435	1	PCT-US95-04439-1
19	603	61.8	1151	1	US-08-286-889-37
20	603	61.8	1151	1	US-08-485-618-37
21	603	61.8	1151	1	US-08-362-652-37
22	603	61.8	1151	2	US-08-605-672-37
23	603	61.8	1151	2	US-08-482-293A-37
24	603	61.8	1151	2	US-08-943-363-37
25	603	61.8	1151	3	US-09-193-043-37
26	603	61.8	1151	4	US-09-688-307A-37
27	603	61.8	1151	4	US-09-350-259-37

28	603	61.8	1161	1	US-08-485-618-55	Sequence 55, Appl
29	603	61.8	1161	1	US-08-362-642-55	Sequence 55, Appl
30	603	61.8	1161	2	US-08-605-672-55	Sequence 55, Appl
31	603	61.8	1161	2	US-08-482-293A-55	Sequence 55, Appl
32	603	61.8	1161	3	US-08-943-363-55	Sequence 55, Appl
33	603	61.8	1161	3	US-09-193-043-55	Sequence 55, Appl
34	603	61.8	1161	4	US-09-688-307A-55	Sequence 55, Appl
35	603	61.8	1161	4	US-09-350-259-55	Sequence 55, Appl
36	602	61.7	413	1	US-08-485-618-101	Sequence 101, App
37	602	61.7	413	2	US-08-605-672-101	Sequence 101, App
38	602	61.7	413	2	US-08-482-293A-101	Sequence 101, App
39	602	61.7	413	2	US-08-943-363-101	Sequence 101, App
40	602	61.7	413	3	US-09-193-043-101	Sequence 101, App
41	602	61.7	413	4	US-09-688-307A-101	Sequence 101, App
42	602	61.7	413	4	US-09-350-259-101	Sequence 101, App
43	594	60.9	1155	1	US-08-286-889-46	Sequence 46, Appl
44	594	60.9	1155	1	US-08-485-618-46	Sequence 46, Appl
45	594	60.9	1155	1	US-08-362-652-46	Sequence 46, Appl

#### ALIGNMENTS

RESULT 1  
US-08-476-062A-43  
Sequence 43, Application US/08476062A  
Patent No. 5877275  
GENERAL INFORMATION:  
APPLICANT: Arnaout, M. Amin  
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY  
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY  
RESPONSES WITH BETA2 INTEGRINS  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,062A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/216,081  
FILING DATE: 21-MAR-1994  
APPLICATION NUMBER: 07/637,830  
FILING DATE: 04-JAN-1991  
APPLICATION NUMBER: 07/539,842  
FILING DATE: 18-JUN-1990  
APPLICATION NUMBER: 07/212,573  
FILING DATE: 28-JUN-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 00786/068003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1152 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-476-062A-43

Query Match 99.8%; Score 974; DB 2; Length 1152;  
Best Local Similarity 99.5%; Pred. No. 1.4e-96;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTLPFSLMOYSEEFRIHFTFK 60  
DB 144 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTLPFSLMOYSEEFRIHFTFK 203  
QY 61 EFQNNPNRSLVKEPIITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120  
DB 204 EFQNNPNRSLVKEPIITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263  
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
QY 181 IONOLREKXFA 191  
DB 324 IONOLREKXIFA 334

## RESULT 2

PCT-US96-01314-43  
Sequence 43, Application PC/TUS9601314  
GENERAL INFORMATION:  
APPLICANT: M. Amin Arnaout  
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN  
TITLE OF INVENTION: ANTAGONISTS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 558X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/01314  
FILING DATE: 30-JAN-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/380,167  
FILING DATE: 30-JAN-95  
ATTORNEY/AGENT INFORMATION:  
NAME: John W. Freeman  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 00786/267001  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1152  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US96-01314-43

Query Match 99.8%; Score 974; DB 2; Length 1152;  
Best Local Similarity 99.5%; Pred. No. 1.4e-96;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTLPFSLMOYSEEFRIHFTFK 60  
DB 144 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTLPFSLMOYSEEFRIHFTFK 203  
QY 61 EFQNNPNRSLVKEPIITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120

DB 204 EFQNNPNRSLVKEPIITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263  
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
QY 181 IONOLREKXFA 191  
DB 324 IONOLREKXIFA 334

## RESULT 3

5424399-2  
Patent No. 5424399  
APPLICANT: ARNAOUT, M. AMIN  
TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS  
NUMBER OF SEQUENCES: 12  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/78,871  
FILING DATE: 16-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 539,842  
FILING DATE: 18-JUN-1990  
APPLICATION NUMBER: 212,573  
FILING DATE: 28-JUN-1988  
SEQ ID NO: 2:  
LENGTH: 1152  
5424399-2

Query Match 99.8%; Score 974; DB 6; Length 1152;  
Best Local Similarity 99.5%; Pred. No. 1.4e-96;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTLPFSLMOYSEEFRIHFTFK 60  
DB 144 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTLPFSLMOYSEEFRIHFTFK 203  
QY 61 EFQNNPNRSLVKEPIITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120  
DB 204 EFQNNPNRSLVKEPIITQLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263  
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
QY 181 IONOLREKXFA 191  
DB 324 IONOLREKXIFA 334

## RESULT 4

5424399-2  
Patent No. 5424399  
APPLICANT: ARNAOUT, M. AMIN  
TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS  
NUMBER OF SEQUENCES: 12  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/78,871  
FILING DATE: 16-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 539,842  
FILING DATE: 18-JUN-1990  
APPLICATION NUMBER: 212,573  
FILING DATE: 28-JUN-1988  
SEQ ID NO: 2:  
LENGTH: 1152  
5424399-2

Query Match 99.8%; Score 974; DB 6; Length 1152;  
Best Local Similarity 99.5%; Pred. No. 1.4e-96;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEOLKSKTLPFSLMOYSEEFRIHFTFK 60

Db 144 CPQSDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEPRIHFTFK 203  
QY 61 EFQNNPNPRLSLVKEPIITQLLGRTHATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120  
Db 204 EFQNNPNPRLSLVKEPIITQLLGRTHATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 263  
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
Db 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
QY 181 IONQLREKXFA 191  
Db 324 IONQLREKXIFA 334

RESULT 5  
US-08-173-497-3  
Sequence 3, Application US/08173497

Patent No. 5437958

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

TITLE OF INVENTION: No. 5437958 Human 2 Integrin Alpha

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 S. Wacker Drive, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,497

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 5437958and, Greca E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/31363

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1153 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-173-497-3

Query Match 99.8%; Score 974; DB 1; Length 1153;

Best Local Similarity 99.5%; Pred. No. 1,4e-96;

Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQSDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEPRIHFTFK 60  
Db 144 CPQSDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEPRIHFTFK 203  
QY 61 EFQNNPNPRLSLVKEPIITQLLGRTHATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120  
Db 204 EFQNNPNPRLSLVKEPIITQLLGRTHATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 263  
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180

Db 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
QY 181 IONQLREKXFA 191  
Db 324 IONQLREKXIFA 334

RESULT 6  
US-08-286-889-3

Sequence 3, Application US/08286889

Patent No. 5470953

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Mich

TITLE OF INVENTION: No. 5470953 Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,889

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: P38,659

REFERENCE/DOCKET NUMBER: 27866/32168

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1153 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-286-889-3

Query Match 99.8%; Score 974; DB 1; Length 1153;

Best Local Similarity 99.5%; Pred. No. 1,4e-96;

Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQSDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEPRIHFTFK 60  
Db 144 CPQSDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEPRIHFTFK 203  
QY 61 EFQNNPNPRLSLVKEPIITQLLGRTHATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120  
Db 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
QY 181 IONQLREKXFA 191  
Db 324 IONQLREKXIFA 334

## RESULT 7

US-08-485-618-3  
; Sequence 3, Application US/08485618  
; Patent No. 5728533  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vieren, Monica  
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Sear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,618  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/362,652  
; FILING DATE: 21-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32797  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1153 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-485-618-3

Query Match 99.8%; Score 974; DB 1; Length 1153;

Best Local Similarity 99.5%; Pred. No. 1.4e-96;

Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLPGLMYSSEFRHIFTFK 60  
DB 144 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLPGLMYSSEFRHIFTFK 203  
QY 61 EFQNNPNRSLVKPTTOLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120  
DB 204 EFQNNPNRSLVKPTTOLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263  
QY 121 DPLGVEDVTPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
DB 264 DPLGVEDVTPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
QY 181 IONQLREKIFA 191  
DB 324 IONQLREKIFA 334

## RESULT 8

## US-08-362-652-3

US-08-362-652-3  
; Sequence 3, Application US/08362652  
; Patent No. 5766850  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vieren, Monica  
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Sear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,652  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32391  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1153 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-362-652-3

Query Match 99.8%; Score 974; DB 1; Length 1153;

Best Local Similarity 99.5%; Pred. No. 1.4e-96;

Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLPGLMYSSEFRHIFTFK 60  
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DB 204 EFQNNPNRSLVKPTTOLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263  
QY 121 DPLGVEDVTPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
DB 264 DPLGVEDVTPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
QY 181 IONQLREKIFA 191  
DB 324 IONQLREKIFA 334

## RESULT 9

US-08-605-672-3  
; Sequence 3, Application US/08605672  
; Patent No. 5817515  
; GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,672  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1153 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-605-672-3

Query Match 99.8%; Score 974; DB 2; Length 1153;  
Best Local Similarity 99.5%; Pred. No. 1,4e-96;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDRMKFVSTVMEOLKSKTLPFLMOYSEEFRIHFTFK 60  
DB 144 CPQEDSDIAFLIDSGSIIIPHDRMKFVSTVMEOLKSKTLPFLMOYSEEFRIHFTFK 203  
QY 61 EFQNNPNRSLVVKITOLLGRTHATGIRKVRRELFNTNGARKNAFKILVITDGEKFG 120  
DB 204 EFQNNPNRSLVVKITOLLGRTHATGIRKVRRELFNTNGARKNAFKILVITDGEKFG 263  
QY 121 DPLGYEDVTPADREGVIRYIVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
DB 264 DPLGYEDVTPADREGVIRYIVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
QY 181 IONOLREKIFA 191  
DB 324 IONOLREKIFA 334

RESULT 10  
US-08-482-293A-3  
Sequence 3, Application US/08482293A  
Patent No. 5831029  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,293A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1153 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-293A-3

Query Match 99.8%; Score 974; DB 2; Length 1153;  
Best Local Similarity 99.5%; Pred. No. 1,4e-96;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDRMKFVSTVMEOLKSKTLPFLMOYSEEFRIHFTFK 60  
DB 144 CPQEDSDIAFLIDSGSIIIPHDRMKFVSTVMEOLKSKTLPFLMOYSEEFRIHFTFK 203  
QY 61 EFQNNPNRSLVVKITOLLGRTHATGIRKVRRELFNTNGARKNAFKILVITDGEKFG 120  
DB 204 EFQNNPNRSLVVKITOLLGRTHATGIRKVRRELFNTNGARKNAFKILVITDGEKFG 263  
QY 121 DPLGYEDVTPADREGVIRYIVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180  
DB 264 DPLGYEDVTPADREGVIRYIVIGVDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323  
QY 181 IONOLREKIFA 191  
DB 324 IONOLREKIFA 334

RESULT 11  
US-08-943-363-3  
Sequence 3, Application US/08943363  
Patent No. 5837478  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vieren, Monica

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; TITLE OF INVENTION: No. 5837478e1 Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,363
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-943-363-3

Query Match          99.8%; Score 974; DB 2; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLPFIMOYSEEFRIHFTFK 60
DB 144 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLPFIMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPTTOLLGRHTATGIRKVRLEFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPTTOLLGRHTATGIRKVRLEFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGVEDVTPADRGVIRYVIGVDAPFRSEKROELNTIAKPRDHVFOVNNFEALKT 180
DB 264 DPLGVEDVTPADRGVIRYVIGVDAPFRSEKROELNTIAKPRDHVFOVNNFEALKT 323
QY 181 IONOLREKXFA 191
DB 324 IONOLREKXFA 334

RESULT 12
US-09-193-043-3
; Sequence 3, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 625195e1 Human 2
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; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193,043
; CURRENT FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-193-043-3

Query Match          99.8%; Score 974; DB 3; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLPFIMOYSEEFRIHFTFK 60
DB 144 CPOEDSDIAFLIDSGSIIIPHDPRMKEFVSTVMEQLKSKTLPFIMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPTTOLLGRHTATGIRKVRLEFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPTTOLLGRHTATGIRKVRLEFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGVEDVTPADRGVIRYVIGVDAPFRSEKROELNTIAKPRDHVFOVNNFEALKT 180
DB 264 DPLGVEDVTPADRGVIRYVIGVDAPFRSEKROELNTIAKPRDHVFOVNNFEALKT 323
QY 181 IONOLREKXFA 191
DB 324 IONOLREKXFA 334

RESULT 13
US-09-688-307A-3
; Sequence 3, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 6432404e1 Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-688-307A-3

Query Match          99.8%; Score 974; DB 4; Length 1153;
Best Local Similarity 99.5%; Pred. No. 1.4e-96;
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Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFRMRKEFVSTVMEQLKSKTLPFSIMQYSEEFRIHFTPK 60  
DB 144 CPQEDSDIAFLIDSGSIIIPHDFRMRKEFVSTVMEQLKSKTLPFSIMQYSEEFRIHFTPK 203  
QY 61 EFQNNPNPRSLVVKPIITQLLGRTHATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120  
DB 204 EFQNNPNPRSLVVKPIITQLLGRTHATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 263  
QY 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180  
DB 264 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 323  
QY 181 IONQLREKXFA 191  
DB 324 IONQLREKXFA 334

## RESULT 14

US-09-350-259-3  
Sequence 3, Application US/09350259  
Patent No. 6620915  
GENERAL INFORMATION:  
APPLICANT: Gallatin, Michael W.  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 6620915el Human 2  
FILE REFERENCE: 27866/35004  
CURRENT APPLICATION NUMBER: US/09/350,259  
EARLIER FILING DATE: 1999-07-08  
EARLIER APPLICATION NUMBER: 08/193,043  
EARLIER FILING DATE: 1998-11-16  
EARLIER APPLICATION NUMBER: 08/173,497  
EARLIER FILING DATE: 1993-12-23  
EARLIER APPLICATION NUMBER: 08/286,889  
EARLIER FILING DATE: 1994-08-05  
EARLIER APPLICATION NUMBER: 08/362,652  
EARLIER FILING DATE: 1994-12-21  
EARLIER APPLICATION NUMBER: 08/943,363  
EARLIER FILING DATE: 1997-10-03  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 1153  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-350-259-3

Query Match 99.8%; Score 974; DB 4; Length 1153;

Best Local Similarity 99.5%; Pred. No. 1.4e-96;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFRMRKEFVSTVMEQLKSKTLPFSIMQYSEEFRIHFTPK 60  
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DB 264 DPLGYEDVPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 323  
QY 181 IONQLREKXFA 191  
DB 324 IONQLREKXFA 334

## RESULT 15

US-08-177-109A-61  
Sequence 61, Application US/08177109A  
Patent No. 5869615

GENERAL INFORMATION:  
APPLICANT: Dennis E. Hourcade and Teresa J. Ogleby  
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/177,109A  
FILING DATE: 03-JAN-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: MU 107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 187 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-177-109A-61

Query Match 98.4%; Score 960; DB 2; Length 187;

Best Local Similarity 100.0%; Pred. No. 4.2e-96;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 EFQNNPNPRSLVVKPIITQLLGRTHATGIRKVVRELFINITNGARKNAFKILVITDGEKFG 120  
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DB 181 IONQLRE 187

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2005, 21:23:19 / Search time 166 Seconds  
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Title: US-09-805-354-1

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Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	974	99.8	191	11	US-09-758-493-1
3	974	99.8	191	14	US-10-144-259-1
4	974	99.8	1152	9	US-09-945-265-4
5	974	99.8	1152	20	US-11-000-473-43
6	974	99.8	1153	3	US-09-350-259-3
7	974	99.8	1153	10	US-09-902-481A-1
8	974	99.8	1153	10	US-09-891-943-3
9	974	99.8	1153	14	US-10-144-259-30
10	974	99.8	1153	14	US-10-207-655-176
11	965	98.9	1137	10	US-09-902-481A-6

12	959	98.3	1137	10	US-09-902-481A-5	Sequence 5, Appl1
13	949	97.2	1137	15	US-09-902-481A-4	Sequence 4, Appl1
14	948	97.1	187	15	US-10-346-863-17	Sequence 37, Appl1
15	948	97.1	187	16	US-10-615-515-9	Sequence 9, Appl1
16	942	96.5	190	15	US-10-346-863-48	Sequence 42, Appl1
17	942	96.5	190	15	US-10-346-863-42	Sequence 48, Appl1
18	942	96.5	216	10	US-09-795-872-5	Sequence 5, Appl1
19	942	96.5	216	16	US-10-662-824-5	Sequence 17, Appl1
20	939	96.2	184	15	US-10-346-863-17	Sequence 3, Appl1
21	936	95.9	1137	10	US-09-902-481A-3	Sequence 11, Appl1
22	745	76.3	199	14	US-10-066-551-11	Sequence 11, Appl1
23	745	76.3	199	16	US-10-665-990A-11	Sequence 37, Appl1
24	603	61.8	1151	9	US-09-350-259-37	Sequence 55, Appl1
25	603	61.8	1151	10	US-09-891-943-37	Sequence 37, Appl1
26	603	61.8	1151	9	US-09-350-259-55	Sequence 55, Appl1
27	603	61.8	1151	10	US-09-891-943-55	Sequence 101, App
28	602	61.7	413	9	US-09-350-259-101	Sequence 101, App
29	602	61.7	413	10	US-09-891-943-101	Sequence 46, Appl1
30	594	60.9	1155	9	US-09-350-259-46	Sequence 53, Appl1
31	594	60.9	1155	10	US-09-891-943-46	Sequence 53, Appl1
32	594	60.9	1151	9	US-09-891-943-53	Sequence 3, Appl1
33	594	60.9	1151	10	US-09-805-354-3	Sequence 3, Appl1
34	591	60.6	191	11	US-09-758-493-3	Sequence 3, Appl1
35	591	60.6	191	11	US-10-144-259-3	Sequence 2, Appl1
36	591	60.6	191	14	US-10-144-259-3	Sequence 2, Appl1
37	591	60.6	1151	9	US-09-350-259-2	Sequence 99, Appl1
38	591	60.6	1151	9	US-09-350-259-99	Sequence 2, Appl1
39	591	60.6	1151	10	US-09-891-943-2	Sequence 99, Appl1
40	591	60.6	1151	10	US-09-891-943-99	Sequence 4, Appl1
41	550	56.4	1153	9	US-09-350-259-4	Sequence 4, Appl1
42	550	56.4	1153	10	US-09-891-943-4	Sequence 2, Appl1
43	548	56.1	191	10	US-09-805-354-2	Sequence 2, Appl1
44	548	56.1	191	11	US-09-758-493-2	Sequence 2, Appl1
45	548	56.1	191	14	US-10-144-259-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1	US-09-805-354-1	Application US/09805354
1	Sequence 1, Appl1	Publication No. US20030078375A1
2	GENERAL INFORMATION:	
3	APPLICANT: Arnaout, M. Amin	
4	APPLICANT: Li, Rui	
5	TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF	
6	FILE REFERENCE: 00786-536001	
7	CURRENT APPLICATION NUMBER: US/09/805,354	
8	CURRENT FILING DATE: 2002-06-04	
9	PRIOR APPLICATION NUMBER: US 09/758,493	
10	PRIOR FILING DATE: 2001-01-11	
11	PRIOR APPLICATION NUMBER: US 60/221,950	
12	PRIOR FILING DATE: 2000-07-31	
13	NUMBER OF SEQ ID NOS: 20	
14	SOFTWARE: FastSeq for Windows Version 4.0	
15	SEQ ID NO 1	
16	LENGTH: 191	
17	TYPE: PRT	
18	ORGANISM: Homo sapiens	
19	US-09-805-354-1	
20	Query Match	99.8%; Score 974; DB 10; Length 191;
21	Best Local Similarity	99.8%; Pred. No. 3.6e-95;
22	Matches 190; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
23	QY	1 CPQEDSDIAFLIDSGSGSIIPHDPFRMKEFVSTWEOUKSKKTLSLMQVSEBRIRHPTFK 60
24	DB	1 CPQEDSDIAFLIDSGSGSIIPHDPFRMKEFVSTWEOUKSKKTLSLMQVSEBRIRHPTFK 60
25	QY	61 EFQNNPRLSLVKRITQLLRTHATGIRKRVLELFINITGARKNAFKILVITDGKFG 120

Db 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120  
QY 121 DPLGYEDVYIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180  
Db 121 DPLGYEDVYIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180  
QY 181 IONQLREKXFA 191  
Db 181 IONQLREKIFA 191

## RESULT 2

US-09-758-493-1  
; Sequence 1, Application US/09758493  
; Publication No. US20040086935A1  
; GENERAL INFORMATION:  
; APPLICANT: Armaout, M. Amin  
; APPLICANT: Li, Rui  
; APPLICANT: Xiong, Jian-Ping  
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND  
; FILE REFERENCE: 00786-804001  
; CURRENT APPLICATION NUMBER: US/09/758,493  
; CURRENT FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: US 60/221,950  
; PRIOR FILING DATE: 2000-07-31  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-493-1

Query Match 99.8%; Score 974; DB 11; Length 191;  
Best Local Similarity 99.5%; Pred. No. 3.6e-95;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60  
Db 1 CPQEDSDIAFLIDSGSIIIPDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60  
QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120  
Db 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120  
QY 121 DPLGYEDVYIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180  
Db 121 DPLGYEDVYIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180  
QY 181 IONQLREKXFA 191  
Db 181 IONQLREKIFA 191

## RESULT 3

US-10-144-259-1  
; Sequence 1, Application US/10144259  
; Publication No. US20030109691A1  
; GENERAL INFORMATION:  
; APPLICANT: Armaout, M. Amin  
; APPLICANT: Li, Rui  
; APPLICANT: Xiong, Jian-Ping  
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: 00786-548001  
; CURRENT APPLICATION NUMBER: US/10/144,259  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: US 09/758,493  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: US 60/221,950  
; PRIOR FILING DATE: 2000-07-31  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-144-259-1

Query Match 99.8%; Score 974; DB 14; Length 191;  
Best Local Similarity 99.5%; Pred. No. 3.6e-95;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60  
Db 1 CPQEDSDIAFLIDSGSIIIPDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60  
QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120  
Db 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120  
QY 121 DPLGYEDVYIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180  
Db 121 DPLGYEDVYIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180  
QY 181 IONQLREKXFA 191  
Db 181 IONQLREKIFA 191

## RESULT 4

US-09-945-265-4  
; Sequence 4, Application US/09945265  
; Patent No. US20020123614A1  
; GENERAL INFORMATION:  
; APPLICANT: Springer, Timothy A.  
; APPLICANT: Shimacka, Motomu  
; APPLICANT: Lu, Chafen  
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A  
; FILE REFERENCE: CBN-002CP  
; CURRENT APPLICATION NUMBER: US/09/945,265  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,700  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1152  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-945-265-4

Query Match 99.8%; Score 974; DB 9; Length 1152;  
Best Local Similarity 99.5%; Pred. No. 4.3e-94;  
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60  
Db 144 CPQEDSDIAFLIDSGSIIIPDFFRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203  
QY 61 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 120  
Db 204 EFQNNPNRSLVKPITQLGRTHTATGIRKVVRELFININGARKNAFKILVITDGEKFG 263  
QY 121 DPLGYEDVYIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 180  
Db 264 DPLGYEDVYIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPRPDHVFQVNNFEALKT 323  
QY 181 IONQLREKXFA 191  
Db 324 IONQLREKIFA 334

## RESULT 5

US-11-000-473-43

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; Sequence 43, Application US/11000473
; Publication No. US20050227296A1
; GENERAL INFORMATION:
; APPLICANT: Amnaut, M. Armin
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS
; FILE REFERENCE: 00786-267002
; CURRENT APPLICATION NUMBER: US/11/000,473
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US/09/592,617
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 08/380,167
; PRIOR FILING DATE: 1999-01-30
; PRIOR APPLICATION NUMBER: US 08/216,081
; PRIOR FILING DATE: 1994-03-21
; PRIOR APPLICATION NUMBER: US 07/637,830
; PRIOR FILING DATE: 1991-01-04
; PRIOR APPLICATION NUMBER: US 07/559,842
; PRIOR FILING DATE: 1990-06-18
; PRIOR APPLICATION NUMBER: US 07/212,573
; PRIOR FILING DATE: 1988-06-28
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -16 to -1
; US-11-000-473-43

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Query Match          99.8%; Score 974; DB 20; Length 1152;
Best Local Similarity 99.5%; Pred. No. 4.3e-94;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CPQEDSDIAFLIDGSGSIIPHDFRPMKEFVSTVMEOLKSKTLPFSLMÖYSEEFRIHFTFK 60
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DB 144 CPQEDSDIAFLIDGSGSIIPHDFRPMKEFVSTVMEOLKSKTLPFSLMÖYSEEFRIHFTFK 203
    |||
QY 61 EFQNNPRLSLVLPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
    |||
DB 204 EFQNNPRLSLVLPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
    |||
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
    |||
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
    |||
QY 181 IQNQLREKXFA 191
    |||
DB 324 IQNQLREKIFA 334
    |||

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RESULT 6
US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. US20020062008A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: NO. US20020062008A1 Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-06-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03

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; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-350-259-3

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Query Match          99.8%; Score 974; DB 9; Length 1153;
Best Local Similarity 99.5%; Pred. No. 4.3e-94;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CPQEDSDIAFLIDGSGSIIPHDFRPMKEFVSTVMEOLKSKTLPFSLMÖYSEEFRIHFTFK 60
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DB 144 CPQEDSDIAFLIDGSGSIIPHDFRPMKEFVSTVMEOLKSKTLPFSLMÖYSEEFRIHFTFK 203
    |||
QY 61 EFQNNPRLSLVLPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
    |||
DB 204 EFQNNPRLSLVLPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
    |||
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
    |||
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
    |||
QY 181 IQNQLREKXFA 191
    |||
DB 324 IQNQLREKIFA 334
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RESULT 7
US-09-902-481A-1

```

```

; Sequence 1, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; APPLICANT: Mayo, Stephen
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/902,481A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (17...)
; OTHER INFORMATION:
; US-09-902-481A-1

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```

Query Match          99.8%; Score 974; DB 10; Length 1153;
Best Local Similarity 99.5%; Pred. No. 4.3e-94;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CPQEDSDIAFLIDGSGSIIPHDFRPMKEFVSTVMEOLKSKTLPFSLMÖYSEEFRIHFTFK 60
    |||
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRPMKEFVSTVMEOLKSKTLPFSLMÖYSEEFRIHFTFK 203
    |||
QY 61 EFQNNPRLSLVLPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
    |||
DB 204 EFQNNPRLSLVLPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
    |||
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
    |||
DB 264 DPLGYEDVPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
    |||
QY 181 IQNQLREKXFA 191
    |||

```



```
/
/
/ TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
/ FILE REFERENCE: A-70586-1/RFT/RMS/RMK
/ CURRENT APPLICATION NUMBER: US/09/902,481A
/ CURRENT FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: US 60/216,600
/ PRIOR FILING DATE: 2000-07-07
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 1137
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic
US-09-902-481A-6

Query Match      98.3%; Score 965; DB 10; Length 1137;
Best Local Similarity 97.4%; Pred. No. 3, 9e-93;
Matches 186; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQLKSKTFLFSIMQYSEEFRIHFTFK 60
DB 128 CPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQLKSKTFLFSIMQYSEEFRIHFTFK 187
QY 61 EFQNNPNRPSLVKPIITQLLGRTHATGIRKVVARELFNTNGARKNAFKLLVITTDGKFG 120
DB 188 EFQNNPNRPSLVKPIITQLLGRTHATGIRKVVARELFNTNGARKNAFKLLVITTDGKFG 247
QY 121 DPLGYEDVTPPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 248 DPLGYEDVTPPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 307
QY 181 IONQLEKXKFA 191
DB 308 IONQLEKXKIFA 318

RESULT 12
US-09-902-481A-5
/ Sequence 5, Application US/09902481A
/ Publication No. US20030054440A1
/ GENERAL INFORMATION:
/ APPLICANT: Springer, Timothy
/ APPLICANT: Shimaoka, Motomu
/ APPLICANT: Shifman, Julia
/ APPLICANT: Mayo, Stephen
/ TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
/ FILE REFERENCE: A-70586-1/RFT/RMS/RMK
/ CURRENT APPLICATION NUMBER: US/09/902,481A
/ CURRENT FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: US 60/216,600
/ PRIOR FILING DATE: 2000-07-07
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 1137
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic
US-09-902-481A-5

Query Match      98.3%; Score 959; DB 10; Length 1137;
Best Local Similarity 95.3%; Pred. No. 1, 7e-92;
Matches 182; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQLKSKTFLFSIMQYSEEFRIHFTFK 60
DB 128 CPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQLKSKTFLFSIMQYSEEFRIHFTFK 187
QY 61 EFQNNPNRPSLVKPIITQLLGRTHATGIRKVVARELFNTNGARKNAFKLLVITTDGKFG 120
DB 188 EFQNNPNRPSLVKPIITQLLGRTHATGIRKVVARELFNTNGARKNAFKLLVITTDGKFG 247
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QY 121 DPLGYEDVTPPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 248 DPLGYEDVTPPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 307
QY 181 IONQLEKXKFA 191
DB 308 IONQLEKXKIFA 318

RESULT 13
US-09-902-481A-4
/ Sequence 4, Application US/09902481A
/ Publication No. US20030054440A1
/ GENERAL INFORMATION:
/ APPLICANT: Springer, Timothy
/ APPLICANT: Shimaoka, Motomu
/ APPLICANT: Shifman, Julia
/ APPLICANT: Mayo, Stephen
/ TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
/ FILE REFERENCE: A-70586-1/RFT/RMS/RMK
/ CURRENT APPLICATION NUMBER: US/09/902,481A
/ CURRENT FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: US 60/216,600
/ PRIOR FILING DATE: 2000-07-07
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 1137
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic
US-09-902-481A-4

Query Match      97.2%; Score 949; DB 10; Length 1137;
Best Local Similarity 94.8%; Pred. No. 4e-91;
Matches 181; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQLKSKTFLFSIMQYSEEFRIHFTFK 60
DB 128 CPQEDSDIAFLIDGSGSIIPHDFRMRKEFVSTVMEQLKSKTFLFSIMQYSEEFRIHFTFK 187
QY 61 EFQNNPNRPSLVKPIITQLLGRTHATGIRKVVARELFNTNGARKNAFKLLVITTDGKFG 120
DB 188 EFQNNPNRPSLVKPIITQLLGRTHATGIRKVVARELFNTNGARKNAFKLLVITTDGKFG 247
QY 121 DPLGYEDVTPPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 248 DPLGYEDVTPPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 307
QY 181 IONQLEKXKFA 191
DB 308 IONQLEKXKIFA 318

RESULT 14
US-10-346-863-37
/ Sequence 37, Application US/10346863
/ Publication No. US20040038325A1
/ GENERAL INFORMATION:
/ APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
/ APPLICANT: FAGAN, RICHARD JOSEPH
/ APPLICANT: GUTTERIDGE, ALEX
/ TITLE OF INVENTION: ADHESION MOLECULES
/ FILE REFERENCE: 674575-2001
/ CURRENT APPLICATION NUMBER: US/10/346,863
/ CURRENT FILING DATE: 2003-01-17
/ PRIOR APPLICATION NUMBER: PCT/GB01/03318
/ PRIOR FILING DATE: 2001-07-24
/ PRIOR APPLICATION NUMBER: GB 0018126.3
/ PRIOR FILING DATE: 2000-07-24
/ PRIOR APPLICATION NUMBER: GB 0025447.4
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;; PRIOR FILING DATE: 2000-10-17  
;; NUMBER OF SEQ ID NOS: 57  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 37  
;; LENGTH: 187  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-346-863-37

Query Match 97.1%; Score 948; DB 15; Length 187;  
Best Local Similarity 99.5%; Pred. No. 2e-92;  
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 DSDIAFLIDGSGSIIIPHDPRRMEKEFVSTVMEQLKSKKTLFSLMOYSEEFRIHFTFKEFON 64  
DB 1 DSDIAFLIDGSGSIIIPHDPRRMEKEFVSTVMEQLKSKKTLFSLMOYSEEFRIHFTFKEFON 60  
OY 65 NPNPRLVKPITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124  
DB 61 NPNPRLVKPITQLGRTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120  
OY 125 YEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIONQ 184  
DB 121 YEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIONQ 180  
OY 185 LREKKFA 191  
DB 181 LREKIFA 187

## RESULT 15

US-10-615-515-9  
; Sequence 9. Application US/10615515  
; Publication No. US20040132974A1  
; GENERAL INFORMATION:  
; APPLICANT: PAGAN, RICHARD, JOSEPH  
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN  
; APPLICANT: GUTTERIDGE, ALEX  
; TITLE OF INVENTION: ADHESION MOLECULES  
; FILE REFERENCE: 674575-2004  
; CURRENT APPLICATION NUMBER: US/10/615,515  
; CURRENT FILING DATE: 2003-07-08  
; PRIOR APPLICATION NUMBER: PCT/GB02/00107  
; PRIOR FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: GB 0100750.9  
; PRIOR FILING DATE: 2001-01-11  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 9  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-615-515-9

Query Match 97.1%; Score 948; DB 16; Length 187;  
Best Local Similarity 99.5%; Pred. No. 2e-92;  
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 185 LREKKFA 191  
DB 181 LREKIFA 187

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